

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	12357	(hepatitis adj c) or hcv-1	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:38
L2	5504	hypervariable adj region	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:38
L3	468	L1 and L2	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:38
L4	56500	E2	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:38
L5	253	L3 and L4	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:38
L6	68191	consensus or motif	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:38
L7	204	L5 and L6	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:38
L8	204	L7	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:39
L9	306	MEFA	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:39
L10	13	l8 and l9	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/07/22 16:39



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for

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Limits Preview/Index **History** Clipboard Details

- Search History will be lost after eight hours of inactivity.
- To combine searches use # before search number, e.g., #2 AND #6.
- Search numbers may not be continuous; all searches are represented.
- Click on query # to add to strategy

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Search	Most Recent Queries	Time	Result
	#8 Related Articles for PubMed (Select 10203493)	16:36:58	185
	#7 Search HCV assay multiple epitope fusion antigen E2	16:36:56	3
	#6 Search HCV assay multiple epitope fusion antigen	16:36:05	5
	#5 Search HCV assay NS3/4a multiple epitope fusion antigen	16:35:53	0
	#4 Search HCV assay NS3/4a MEFA	16:35:42	0
	#3 Search HCV assay NS3/4a	16:35:29	24
	#2 Search hepatitis C or HCV assay	16:35:07	35765
	#1 Search hepatitis C or HCV	16:35:03	36742

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Jul 17 2006 06:31:01



NCBI

results of BLAST**BLASTP 2.2.14 [May-07-2006]****Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference:

Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

RID: 1153601903-10757-200512290520.BLASTQ4

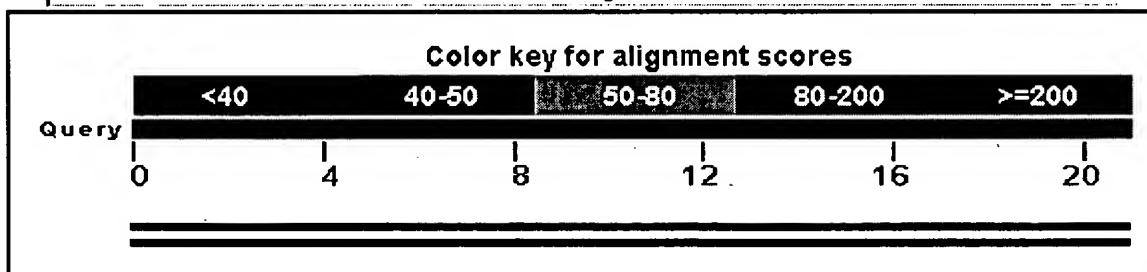
Database: NCBI Protein Reference Sequences
2,389,055 sequences; 864,113,167 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=21

Distribution of 2 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments

**Distance tree of results** [NEW]

Sequences producing significant alignments:	Score (Bits)	E Value	
gi 26053623 ref NP_751921.1 E2 protein; viral envelope protein	34.7	0.60	
gi 22129793 ref NP_671491.1 polyprotein [Hepatitis C virus]	34.3	1.0	

Alignments

[Get selected sequences](#)[Select all](#)[Deselect all](#)[Distance tree of results](#)

> gi|26053623|ref|NP_751921.1| G E2 protein; viral envelope protein [Hepatitis C virus]
Length=363

Score = 34.7 bits (78), Expect = 0.60, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RTT+G V L PGAKQN
Sbjct 7 GSAGRRTAGLVGLLTPGAKQN 27

> gi|22129793|ref|NP_671491.1| G polyprotein [Hepatitis C virus]
Length=3011

Score = 34.3 bits (77), Expect = 1.0, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RTT+G V L PGAKQN
Sbjct 390 GSAGRRTAGLVGLLTPGAKQN 410

[Get selected sequences](#)[Select all](#)[Deselect all](#)[Distance tree of results](#)

Database: NCBI Protein Reference Sequences
Posted date: Jul 21, 2006 3:13 AM
Number of letters in database: 864,113,167
Number of sequences in database: 2,389,055
Lambda K H
0.311 0.123 0.341
Gapped
Lambda K H
0.267 0.0410 0.140
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 2389055
Number of Hits to DB: 6542300
Number of extensions: 52324
Number of successful extensions: 36
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 36
Number of HSP's successfully gapped: 0
Length of query: 21
Length of database: 864113167
Length adjustment: 0
Effective length of query: 21
Effective length of database: 864113167
Effective search space: 18146376507
Effective search space used: 18146376507
T: 11
A: 40
X1: 16 (7.2 bits)
X2: 38 (14.6 bits)



results of BLAST

BLASTP 2.2.14 [May-07-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference:

Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

RID: 1153601814-24595-124256429206.BLASTQ4

Database: pat

301,733 sequences; 55,455,050 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

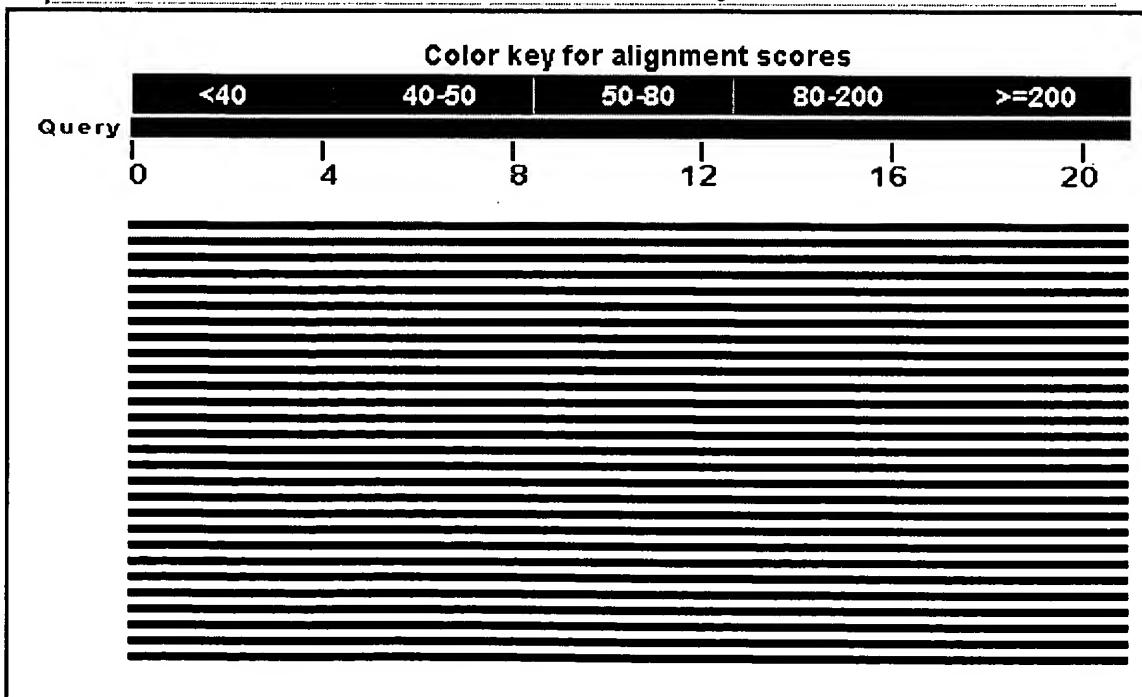
[Taxonomy reports](#)

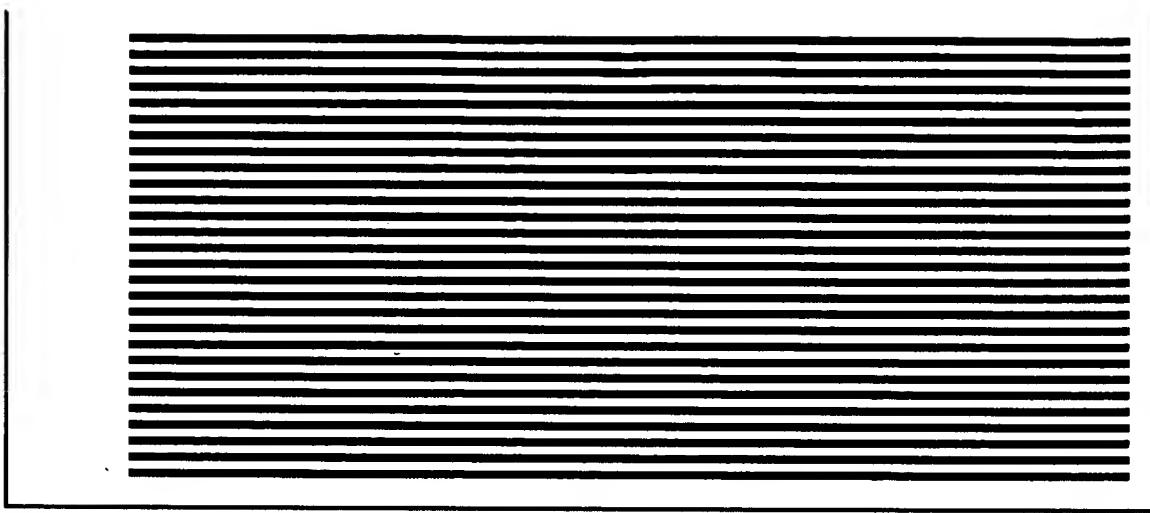
Query=

Length=21

Distribution of 103 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments



Distance tree of results NEW

Sequences producing significant alignments:	Score (Bits)	E Value
<u>gi 56627909 gb AAW06245.1 </u> Sequence 4 from patent US 6797809 ...	<u>43.1</u>	<u>1e-04</u>
<u>gi 40153769 gb AAR65055.1 </u> Sequence 5 from patent US 6630298 ...	<u>42.0</u>	<u>2e-04</u>
<u>gi 20221594 gb AAE87167.1 </u> Sequence 3 from patent US 6326171 ...	<u>38.1</u>	<u>0.003</u>
<u>gi 33759571 gb AAQ52061.1 </u> Sequence 35 from patent US 6593083...	<u>38.1</u>	<u>0.004</u>
<u>gi 33759570 gb AAQ52060.1 </u> Sequence 34 from patent US 6593083...	<u>37.7</u>	<u>0.005</u>
<u>gi 17912916 gb AAE83170.1 </u> Sequence 14 from patent US 6303292...	<u>37.7</u>	<u>0.005</u>
<u>gi 3993851 gb AAC87279.1 AR007645</u> Sequence 13 from patent US ...	<u>37.7</u>	<u>0.005</u>
<u>gi 15108282 gb AAE67318.1 </u> Sequence 39 from patent US 6210962...	<u>37.4</u>	<u>0.006</u>
<u>gi 56567645 gb AAV98707.1 </u> Sequence 7 from patent US 6740323 ...	<u>37.0</u>	<u>0.008</u>
<u>gi 14101409 gb AAE53726.1 </u> Sequence 89 from patent US 6150087	<u>37.0</u>	<u>0.009</u>
<u>gi 31689077 gb AAP61048.1 </u> Sequence 2 from patent US 6538123 ...	<u>36.6</u>	<u>0.011</u>
<u>gi 593530 gb AAA55137.1 </u> Sequence 2 from Patent EP 0388232	<u>36.6</u>	<u>0.011</u>
<u>gi 21508650 gb AAM58139.1 </u> Sequence 1 from patent US 6379886	<u>36.6</u>	<u>0.011</u>
<u>gi 16239032 gb AAE78869.1 </u> Sequence 3 from patent US 6274148 ...	<u>36.6</u>	<u>0.011</u>
<u>gi 14101433 gb AAE53750.1 </u> Sequence 138 from patent US 6150087	<u>36.6</u>	<u>0.011</u>
<u>gi 14101424 gb AAE53741.1 </u> Sequence 124 from patent US 6150087	<u>36.6</u>	<u>0.011</u>
<u>gi 14124296 gb AAE60492.1 </u> Sequence 6 from patent US 6194140 ...	<u>36.6</u>	<u>0.011</u>
<u>gi 33759567 gb AAQ52057.1 </u> Sequence 31 from patent US 6593083...	<u>36.2</u>	<u>0.014</u>
<u>gi 14101452 gb AAE53769.1 </u> Sequence 175 from patent US 6150087	<u>35.4</u>	<u>0.023</u>
<u>gi 33737406 gb AAQ41059.1 </u> Sequence 23 from patent US 6576417...	<u>35.4</u>	<u>0.026</u>
<u>gi 14101440 gb AAE53757.1 </u> Sequence 157 from patent US 6150087	<u>35.4</u>	<u>0.026</u>
<u>gi 3993852 gb AAC87280.1 AR007646</u> Sequence 15 from patent US ...	<u>35.0</u>	<u>0.033</u>
<u>gi 17912926 gb AAE83180.1 </u> Sequence 24 from patent US 6303292...	<u>35.0</u>	<u>0.036</u>
<u>gi 14101405 gb AAE53722.1 </u> Sequence 81 from patent US 6150087	<u>34.7</u>	<u>0.039</u>
<u>gi 40114092 gb AAR55231.1 </u> Sequence 180 from patent US 661333...	<u>34.7</u>	<u>0.041</u>
<u>gi 91149569 gb ABE23184.1 </u> Sequence 2 from patent US 7009044	<u>34.7</u>	<u>0.047</u>
<u>gi 33759566 gb AAQ52056.1 </u> Sequence 30 from patent US 6593083...	<u>34.3</u>	<u>0.058</u>
<u>gi 14101441 gb AAE53758.1 </u> Sequence 158 from patent US 6150087	<u>34.3</u>	<u>0.064</u>
<u>gi 91165235 gb ABE25678.1 </u> Sequence 3 from patent US 7022323	<u>34.3</u>	<u>0.064</u>
<u>gi 12828946 gb AAE50646.1 </u> Sequence 2 from patent US 6127116	<u>34.3</u>	<u>0.064</u>
<u>gi 14101448 gb AAE53765.1 </u> Sequence 171 from patent US 6150087	<u>33.9</u>	<u>0.074</u>
<u>gi 15108283 gb AAE67319.1 </u> Sequence 40 from patent US 6210962...	<u>33.9</u>	<u>0.075</u>
<u>gi 40114093 gb AAR55232.1 </u> Sequence 181 from patent US 661333...	<u>33.9</u>	<u>0.081</u>
<u>gi 77153553 emb CAJ33637.1 </u> unnamed protein product [synthetic c	<u>33.9</u>	<u>0.082</u>
<u>gi 77153498 emb CAJ33635.1 </u> unnamed protein product [synthetic c	<u>33.5</u>	<u>0.088</u>
<u>gi 3993854 gb AAC87282.1 AR007648</u> Sequence 19 from patent US ...	<u>33.5</u>	<u>0.091</u>
<u>gi 17912919 gb AAE83173.1 </u> Sequence 17 from patent US 6303292...	<u>33.5</u>	<u>0.092</u>
<u>gi 17912922 gb AAE83176.1 </u> Sequence 20 from patent US 6303292...	<u>33.5</u>	<u>0.095</u>

gi 15108276 gb AAE67312.1	Sequence 5 from patent US 6210962 ...	33.5	0.099
gi 17912933 gb AAE83187.1	Sequence 31 from patent US 6303292...	33.5	0.10
gi 77153551 emb CAJ33636.1	unnamed protein product [unidentifie	33.1	0.11
gi 6001419 gb AAE22381.1	Sequence 4 from patent US 5854001 >...	33.1	0.11
gi 42685373 gb AAS29954.1	Sequence 4 from patent US 6680059 ...	33.1	0.13
gi 77153496 emb CAJ33634.1	unnamed protein product [Hepatitis C	33.1	0.14
gi 75915319 gb ABA29873.1	Sequence 20 from patent US 6921634...	32.7	0.16
gi 42685370 gb AAS29951.1	Sequence 1 from patent US 6680059 ...	32.7	0.18
gi 2492381 gb AAB80517.1 I58189	Sequence 13 from patent US 56100	32.7	0.19
gi 2492387 gb AAB80523.1 I58195	Sequence 19 from patent US 56100	32.3	0.21
gi 2492389 gb AAB80525.1 I58197	Sequence 21 from patent US 56100	32.3	0.22
gi 51997479 emb CAH33883.1	unnamed protein product [syntheti...	32.3	0.23
gi 2492384 gb AAB80520.1 I58192	Sequence 16 from patent US 56100	32.3	0.24
gi 2492383 gb AAB80519.1 I58191	Sequence 15 from patent US 56100	32.3	0.24
gi 17912934 gb AAE83188.1	Sequence 32 from patent US 6303292...	32.0	0.25
gi 51997481 emb CAH33884.1	unnamed protein product [syntheti...	32.0	0.25
gi 6001417 gb AAE22379.1	Sequence 1 from patent US 5854001 >...	32.0	0.26
gi 12828947 gb AAE50647.1	Sequence 20 from patent US 6127116	32.0	0.28
gi 6001418 gb AAE22380.1	Sequence 2 from patent US 5854001 >...	32.0	0.28
gi 6001422 gb AAE22384.1	Sequence 10 from patent US 5854001 ...	32.0	0.28
gi 2492388 gb AAB80524.1 I58196	Sequence 20 from patent US 56100	32.0	0.28
gi 2492386 gb AAB80522.1 I58194	Sequence 18 from patent US 56100	32.0	0.28
gi 17912925 gb AAE83179.1	Sequence 23 from patent US 6303292...	32.0	0.29
gi 6001420 gb AAE22382.1	Sequence 6 from patent US 5854001 >...	32.0	0.29
gi 3992567 gb AAC85994.1 AR005511	Sequence 89 from patent US 574	32.0	0.29
gi 2492380 gb AAB80516.1 I58188	Sequence 12 from patent US 56100	32.0	0.32
gi 2492376 gb AAB80512.1 I58184	Sequence 7 from patent US 561000	31.6	0.32
gi 3993850 gb AAC87278.1 AR007644	Sequence 11 from patent US ...	31.6	0.37
gi 3992566 gb AAC85993.1 AR005510	Sequence 88 from patent US 574	31.6	0.37
gi 40114091 gb AAR55230.1	Sequence 179 from patent US 661333...	31.2	0.45
gi 3992568 gb AAC85995.1 AR005512	Sequence 90 from patent US 574	31.2	0.47
gi 6001423 gb AAE22385.1	Sequence 12 from patent US 5854001 ...	30.8	0.60
gi 33759563 gb AAQ52053.1	Sequence 24 from patent US 6593083...	30.8	0.64
gi 14101437 gb AAE53754.1	Sequence 150 from patent US 6150087	30.4	0.75
gi 14101439 gb AAE53756.1	Sequence 156 from patent US 6150087	30.4	0.85
gi 14101449 gb AAE53766.1	Sequence 172 from patent US 6150087	30.0	1.1
gi 75915326 gb ABA29880.1	Sequence 40 from patent US 6921634	29.3	1.8
gi 33767210 gb AAQ52972.1	Sequence 16 from patent US 6596476	28.9	2.2
gi 91126690 gb ABE13381.1	Sequence .80 from patent US 6977144	28.9	2.3
gi 3992487 gb AAC85914.1 AR005431	Sequence 9 from patent US 5747	28.9	2.5
gi 42713600 gb AAS36747.1	Sequence 50 from patent US 6692907...	28.9	2.5
gi 40114102 gb AAR55240.1	Sequence 189 from patent US 661333...	28.9	2.6
gi 42713619 gb AAS36766.1	Sequence 69 from patent US 6692907	28.1	4.4
gi 911719 gb AAA71173.1	Sequence 8 from patent US 5428145	28.1	4.4
gi 16219211 gb AAE73970.1	Sequence 36 from patent US 6245503...	28.1	4.4
gi 16219221 gb AAE73976.1	Sequence 48 from patent US 6245503...	27.7	4.8
gi 14101438 gb AAE53755.1	Sequence 152 from patent US 6150087	27.7	5.0
gi 40160957 gb AAR67309.1	Sequence 30 from patent US 6635257...	27.7	5.3
gi 16219219 gb AAE73975.1	Sequence 46 from patent US 6245503...	27.7	5.4
gi 42713683 gb AAS36830.1	Sequence 133 from patent US 6692907	27.7	5.5
gi 42713552 gb AAS36699.1	Sequence 2 from patent US 6692907	27.7	5.5
gi 16219215 gb AAE73973.1	Sequence 42 from patent US 6245503...	27.7	5.7
gi 42669271 gb AAS24964.1	Sequence 4 from patent US 6670114	27.7	6.0
gi 16219223 gb AAE73977.1	Sequence 50 from patent US 6245503...	27.3	6.3
gi 16219212 gb AAE73971.1	Sequence 38 from patent US 6245503...	27.3	7.2
gi 40114103 gb AAR55241.1	Sequence 190 from patent US 661333...	27.3	7.4
gi 4529993 emb CAA03144.1	unnamed protein product [unidentified	27.3	7.6
gi 29370898 emb CAD86508.1	unnamed protein product [synthetic c	27.3	7.8
gi 2492379 gb AAB80515.1 I58187	Sequence 11 from patent US 56100	27.3	7.8
gi 16219217 gb AAE73974.1	Sequence 44 from patent US 6245503...	27.3	7.9
gi 12824387 gb AAE49293.1	Sequence 93 from patent US 6110465	27.3	7.9

<u>gi 2492378 gb AAB80514.1 I58186</u>	Sequence 10 from patent US 56100	27.3	7.9
<u>gi 16219213 gb AAE73972.1 </u>	Sequence 40 from patent US 6245503...	26.9	7.9
<u>gi 40114118 gb AAR55252.1 </u>	Sequence 201 from patent US 661333...	26.9	8.3
<u>gi 3992565 gb AAC85992.1 AR005509</u>	Sequence 87 from patent US 574	26.9	8.5
<u>gi 2492385 gb AAB80521.1 I58193</u>	Sequence 17 from patent US 56100	26.9	9.5
<u>gi 14103322 gb AAE54756.1 </u>	Sequence 5 from patent US 6153421	26.9	9.8

Alignments

Get selected sequences Select all Deselect all Distance tree of results

> gi|56627909|gb|AAW06245.1| Sequence 4 from patent US 6797809
gi|40158517|gb|AAR66374.1| Sequence 4 from patent US 6632601
gi|21714050|emb|CAD38233.1| unnamed protein product [synthetic construct]
Length=1099

Score = 43.1 bits (100), Expect = 1e-04, Method: Composition-based stats.
Identities = 21/21 (100%), Positives = 21/21 (100%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTSGFVSLFAPGAKQN
Sbjct 179 GSAARTTSGFVSLFAPGAKQN 199

Score = 35.4 bits (80), Expect = 0.022, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+AARTTSG SLF+PGA QN
Sbjct 206 GAAARTTSGLTSLFSPGASQN 226

> gi|40153769|gb|AAR65055.1| Sequence 5 from patent US 6630298
gi|21066311|emb|CAD32155.1| unnamed protein product [synthetic construct]
Length=829

Score = 42.0 bits (97), Expect = 2e-04, Method: Composition-based stats.
Identities = 21/21 (100%), Positives = 21/21 (100%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTSGFVSLFAPGAKQN
Sbjct 92 GSAARTTSGFVSLFAPGAKQN 112

Score = 34.7 bits (78), Expect = 0.039, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+AARTTSG SLF+PGA QN
Sbjct 119 GAAARTTSGLTSLFSPGASQN 139

> gi|20221594|gb|AAE87167.1| Sequence 3 from patent US 6326171
gi|29718028|gb|AAP01124.1| Sequence 4 from patent US 6521423
Length=663

Score = 38.1 bits (87), Expect = 0.003, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)



results of BLAST

BLASTP 2.2.14 [May-07-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference:

Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

RID: 1153601291-14310-20277516180.BLASTQ1

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples
 3,807,609 sequences; 1,312,719,415 total letters

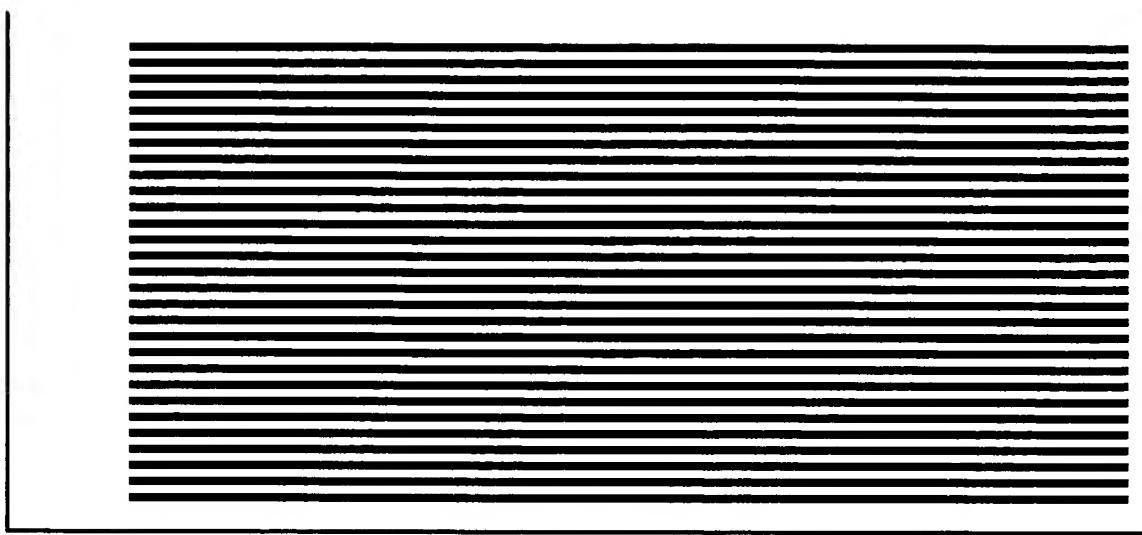
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[Taxonomy reports](#)

Query=
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Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments



Distance tree of results NEW

Sequences producing significant alignments:	Score (Bits)	E Value
gi 58198305 gb AAW65860.1 envelope protein [synthetic construct]	41.2	0.010
gi 64501453 gb AYY41694.1 envelope [Hepatitis C virus]	41.2	0.011
gi 58198313 gb AAW65864.1 envelope protein [synthetic construct]	41.2	0.011
gi 58198309 gb AAW65862.1 envelope protein [synthetic construct]	41.2	0.011
gi 64501451 gb AYY41693.1 envelope [Hepatitis C virus]	41.2	0.011
gi 64501435 gb AYY41685.1 envelope [Hepatitis C virus]	41.2	0.012
gi 58198311 gb AAW65863.1 envelope protein [synthetic construct]	41.2	0.012
gi 64501449 gb AYY41692.1 envelope [Hepatitis C virus]	41.2	0.012
gi 64501447 gb AYY41691.1 envelope [Hepatitis C virus]	41.2	0.012
gi 2565261 gb AAC61802.1 E2/NS1 protein [Hepatitis C virus]	39.7	0.030
gi 15341438 gb AAK95634.1 polyprotein [Hepatitis C virus]	39.7	0.031
gi 58220842 gb AAW68049.1 envelope protein [synthetic construct]	39.3	0.037
gi 64501419 gb AYY41677.1 envelope [Hepatitis C virus] >gi 6...	39.3	0.042
gi 64501423 gb AYY41679.1 envelope [Hepatitis C virus]	39.3	0.044
gi 64501439 gb AYY41687.1 envelope [Hepatitis C virus]	39.3	0.044
gi 64501427 gb AYY41681.1 envelope [Hepatitis C virus]	39.3	0.044
gi 64501445 gb AYY41690.1 envelope [Hepatitis C virus]	39.3	0.046
gi 13448566 gb AAK27104.1 polyprotein [Hepatitis C virus]	38.1	0.099
gi 58198307 gb AAW65861.1 envelope protein [synthetic construct]	37.7	0.13
gi 64501455 gb AYY41695.1 envelope [Hepatitis C virus]	37.7	0.13
gi 64501429 gb AYY41682.1 envelope [Hepatitis C virus]	37.7	0.14
gi 33337015 gb AAQ13175.1 polyprotein [Hepatitis C virus]	37.0	0.20
gi 64501425 gb AYY41680.1 truncated envelope [Hepatitis C vi...]	37.0	0.20
gi 53801738 gb AAU94042.1 polyprotein [Hepatitis C virus] >g...	37.0	0.21
gi 16518692 gb AAL24947.1 glycoprotein [Hepatitis C virus]	37.0	0.23
gi 13448510 gb AAK27077.1 polyprotein [Hepatitis C virus].	37.0	0.23
gi 33337023 gb AAQ13179.1 polyprotein [Hepatitis C virus]	36.6	0.24
gi 53801728 gb AAU94037.1 polyprotein [Hepatitis C virus]	36.6	0.25
gi 13448516 gb AAK27080.1 polyprotein [Hepatitis C virus]	36.6	0.25
gi 130455 sp P26664 POLG_HCV1 Genome polyprotein [Contains: C...	36.6	0.26
gi 67810851 gb AYY82013.1 polyprotein [Hepatitis C virus]	36.6	0.26
gi 67810849 gb AYY82012.1 polyprotein [Hepatitis C virus]	36.6	0.26
gi 14532249 gb AAK66556.1 HCV type 1a/1b chimera polyprotein...	36.6	0.26
gi 14532251 gb AAK66557.1 HCV type 1a/1b chimera mutant polypro	36.6	0.26
gi 53801732 gb AAU94039.1 polyprotein [Hepatitis C virus]	36.6	0.27
gi 33337057 gb AAQ13196.1 polyprotein [Hepatitis C virus] >g...	36.6	0.28
gi 37957242 gb AAP03950.1 polyprotein [Hepatitis C virus]	36.6	0.28

gi 436988 gb AAA45601.1	putative		36.6	0.28
gi 7649227 gb AAF65803.1	polyprotein precursor [Hepatitis C virus]		36.6	0.30
gi 37957231 gb AAP03945.1	polyprotein [Hepatitis C virus]		36.2	0.32
gi 33337017 gb AAQ13176.1	polyprotein [Hepatitis C virus]		36.2	0.32
gi 33337005 gb AAQ13170.1	polyprotein [Hepatitis C virus]		36.2	0.32
gi 67810855 gb AYY82015.1	polyprotein [Hepatitis C virus]		36.2	0.32
gi 67810853 gb AYY82014.1	polyprotein [Hepatitis C virus]		36.2	0.32
gi 13448514 gb AAK27079.1	polyprotein [Hepatitis C virus]		36.2	0.33
gi 7670859 gb AAF66249.1	polyprotein precursor [Hepatitis C virus]		36.2	0.34
gi 33336981 gb AAQ13158.1	polyprotein [Hepatitis C virus]		36.2	0.34
gi 4469531 gb AAD21305.1	polyprotein [Hepatitis C virus]		36.2	0.34
gi 33337045 gb AAQ13190.1	polyprotein [Hepatitis C virus]		36.2	0.36
gi 13448244 gb AAK26946.1	polyprotein [Hepatitis C virus]		36.2	0.36
gi 33337025 gb AAQ13180.1	polyprotein [Hepatitis C virus]		36.2	0.36
gi 33337021 gb AAQ13178.1	polyprotein [Hepatitis C virus]		36.2	0.36
gi 33336921 gb AAQ13128.1	polyprotein [Hepatitis C virus]		36.2	0.36
gi 53802198 gb AAU94270.1	polyprotein [Hepatitis C virus]		36.2	0.38
gi 13448555 gb AAK27099.1	polyprotein [Hepatitis C virus]		36.2	0.39
gi 33336927 gb AAQ13131.1	polyprotein [Hepatitis C virus]		36.2	0.39
gi 37957251 gb AAP03954.1	polyprotein [Hepatitis C virus]		36.2	0.40
gi 37957229 gb AAP03944.1	polyprotein [Hepatitis C virus]		36.2	0.40
gi 33336925 gb AAQ13130.1	polyprotein [Hepatitis C virus] >gi...		36.2	0.40
gi 33336495 gb AAQ12915.1	polyprotein [Hepatitis C virus]		36.2	0.40
gi 33337001 gb AAQ13168.1	polyprotein [Hepatitis C virus]		35.8	0.40
gi 13344963 gb AAK19135.1	polyprotein precursor [Hepatitis C vi		35.8	0.41
gi 7670871 gb AAF66255.1	polyprotein precursor [Hepatitis C vir		35.8	0.41
gi 53802217 gb AAU94278.1	polyprotein [Hepatitis C virus]		35.8	0.41
gi 33336881 gb AAQ13108.1	polyprotein [Hepatitis C virus]		35.8	0.41
gi 37957244 gb AAP03951.1	polyprotein [Hepatitis C virus]		35.8	0.41
gi 37957239 gb AAP03949.1	polyprotein [Hepatitis C virus] >gi...		35.8	0.42
gi 33336889 gb AAQ13112.1	polyprotein [Hepatitis C virus]		35.8	0.42
gi 13448238 gb AAK26943.1	polyprotein [Hepatitis C virus]		35.8	0.42
gi 7670919 gb AAF66279.1	polyprotein precursor [Hepatitis C vir		35.8	0.42
gi 7670867 gb AAF66253.1	polyprotein precursor [Hepatitis C vir		35.8	0.42
gi 33336867 gb AAQ13101.1	polyprotein [Hepatitis C virus] >gi...		35.8	0.43
gi 33336885 gb AAQ13110.1	polyprotein [Hepatitis C virus]		35.8	0.44
gi 16518684 gb AAL24943.1	glycoprotein [Hepatitis C virus]		35.8	0.44
gi 7670861 gb AAF66250.1	polyprotein precursor [Hepatitis C vir		35.8	0.44
gi 7670939 gb AAF66289.1	polyprotein precursor [Hepatitis C vir		35.8	0.45
gi 33336909 gb AAQ13122.1	polyprotein [Hepatitis C virus]		35.8	0.47
gi 4927491 gb AAD33137.1	polyprotein [Hepatitis C virus]		35.8	0.47
gi 37957257 gb AAP03957.1	polyprotein [Hepatitis C virus]		35.8	0.48
gi 13448474 gb AAK27059.1	polyprotein [Hepatitis C virus]		35.8	0.49
gi 37957255 gb AAP03956.1	polyprotein [Hepatitis C virus]		35.8	0.50
gi 13448502 gb AAK27073.1	polyprotein [Hepatitis C virus]		35.8	0.50
gi 37957179 gb AAP03919.1	polyprotein [Hepatitis C virus]		35.8	0.50
gi 13448524 gb AAK27084.1	polyprotein [Hepatitis C virus]		35.8	0.51
gi 37957249 gb AAP03953.1	polyprotein [Hepatitis C virus]		35.8	0.52
gi 37957246 gb AAP03952.1	polyprotein [Hepatitis C virus]		35.8	0.52
gi 33336887 gb AAQ13111.1	polyprotein [Hepatitis C virus]		35.8	0.52
gi 53801742 gb AAU94044.1	polyprotein [Hepatitis C virus]		35.8	0.52
gi 4927589 gb AAD33166.1	polyprotein [Hepatitis C virus]		35.4	0.55
gi 4927496 gb AAD33142.1	polyprotein [Hepatitis C virus] >gi...		35.4	0.55
gi 53801730 gb AAU94038.1	polyprotein [Hepatitis C virus]		35.4	0.55
gi 51558189 gb AAU06654.1	envelope glycoprotein [Hepatitis C vi		35.4	0.56
gi 53801726 gb AAU94036.1	polyprotein [Hepatitis C virus]		35.4	0.56
gi 53801734 gb AAU94040.1	polyprotein [Hepatitis C virus]		35.4	0.57
gi 33336863 gb AAQ13099.1	polyprotein [Hepatitis C virus]		35.4	0.57
gi 38539525 gb AAR23635.1	polyprotein [Hepatitis C virus]		35.4	0.58
gi 221688 dbj BAA14118.1	X protein [Hepatitis C virus]		35.4	0.58
gi 37957233 gb AAP03946.1	polyprotein [Hepatitis C virus]		35.4	0.59

gi 53801718 gb AAU94032.1	polyprotein [Hepatitis C virus]	35.4	0.59
gi 33336821 gb AAQ13078.1	polyprotein [Hepatitis C virus]	35.4	0.59
gi 4927621 gb AAD33198.1	polyprotein [Hepatitis C virus]	35.4	0.60
gi 4927579 gb AAD33156.1	polyprotein [Hepatitis C virus]	35.4	0.63
gi 33336839 gb AAQ13087.1	polyprotein [Hepatitis C virus]	35.4	0.64
gi 7670905 gb AAF66272.1	polyprotein precursor [Hepatitis C vir	35.4	0.64
gi 13448551 gb AAK27097.1	polyprotein [Hepatitis C virus]	35.4	0.66
gi 13344959 gb AAK19133.1	polyprotein precursor [Hepatitis C vi	35.4	0.66
gi 33336865 gb AAQ13100.1	polyprotein [Hepatitis C virus]	35.4	0.66
gi 16518694 gb AAL24948.1	glycoprotein [Hepatitis C virus] >...	35.4	0.67
gi 13448545 gb AAK27094.1	polyprotein [Hepatitis C virus] >g...	35.4	0.67
gi 13448541 gb AAK27092.1	polyprotein [Hepatitis C virus]	35.4	0.67
gi 33336851 gb AAQ13093.1	polyprotein [Hepatitis C virus]	35.0	0.70
gi 13448539 gb AAK27091.1	polyprotein [Hepatitis C virus]	35.0	0.71
gi 33336931 gb AAQ13133.1	polyprotein [Hepatitis C virus] >g...	35.0	0.71
gi 4927584 gb AAD33161.1	polyprotein [Hepatitis C virus]	35.0	0.71
gi 4927575 gb AAD33152.1	polyprotein [Hepatitis C virus]	35.0	0.71
gi 53801809 gb AAU94077.1	polyprotein [Hepatitis C virus]	35.0	0.72
gi 53801937 gb AAU94141.1	polyprotein [Hepatitis C virus]	35.0	0.73
gi 221587 dbj BAA01582.1	polyprotein precursor [Hepatitis C vir	35.0	0.76
gi 13448316 gb AAK26981.1	polyprotein [Hepatitis C virus] >g...	35.0	0.77
gi 33336823 gb AAQ13079.1	polyprotein [Hepatitis C virus]	35.0	0.77
gi 13448620 gb AAK27131.1	polyprotein [Hepatitis C virus]	35.0	0.77
gi 33336861 gb AAQ13098.1	polyprotein [Hepatitis C virus] >g...	35.0	0.79
gi 53801951 gb AAU94147.1	polyprotein [Hepatitis C virus]	35.0	0.79
gi 13448549 gb AAK27096.1	polyprotein [Hepatitis C virus]	35.0	0.80
gi 13448320 gb AAK26983.1	polyprotein [Hepatitis C virus]	35.0	0.80
gi 13448588 gb AAK27115.1	polyprotein [Hepatitis C virus] >g...	35.0	0.81
gi 53802206 gb AAU94273.1	polyprotein [Hepatitis C virus]	35.0	0.81
gi 89519415 gb ABD75829.1	polyprotein [Hepatitis C virus]	35.0	0.81
gi 33336965 gb AAQ13150.1	polyprotein [Hepatitis C virus]	35.0	0.82
gi 13448326 gb AAK26986.1	polyprotein [Hepatitis C virus]	35.0	0.82
gi 33337033 gb AAQ13184.1	polyprotein [Hepatitis C virus]	35.0	0.83
gi 13448314 gb AAK26980.1	polyprotein [Hepatitis C virus]	35.0	0.84
gi 56406500 gb AAV87599.1	polyprotein [Hepatitis C virus]	35.0	0.85
gi 33336761 gb AAQ13048.1	polyprotein [Hepatitis C virus]	35.0	0.85
gi 13448578 gb AAK27110.1	polyprotein [Hepatitis C virus]	35.0	0.86
gi 33637194 gb AAQ23753.1	polyprotein [Hepatitis C virus]	35.0	0.86
gi 33336525 gb AAQ12930.1	polyprotein [Hepatitis C virus]	35.0	0.87
gi 13448322 gb AAK26984.1	polyprotein [Hepatitis C virus]	35.0	0.87
gi 33336639 gb AAQ12987.1	polyprotein [Hepatitis C virus]	35.0	0.89
gi 13448318 gb AAK26982.1	polyprotein [Hepatitis C virus]	35.0	0.89
gi 53801935 gb AAU94140.1	polyprotein [Hepatitis C virus]	35.0	0.89
gi 33336815 gb AAQ13075.1	polyprotein [Hepatitis C virus]	35.0	0.89
gi 7649241 gb AAF65810.1	polyprotein precursor [Hepatitis C vir	34.7	0.90
gi 109259768 gb AAW65879.2	envelope protein [synthetic construc	34.7	0.90
gi 13448296 gb AAK26971.1	polyprotein [Hepatitis C virus]	34.7	0.91
gi 13448294 gb AAK26970.1	polyprotein [Hepatitis C virus]	34.7	0.91
gi 53801948 gb AAU94146.1	polyprotein [Hepatitis C virus]	34.7	0.91
gi 26053623 ref NP_751921.1	E2 protein; viral envelope protein	34.7	0.91
gi 13448580 gb AAK27111.1	polyprotein [Hepatitis C virus]	34.7	0.92
gi 64501433 gb AYY41684.1	envelope [Hepatitis C virus]	34.7	0.92
gi 37957282 gb AAP03969.1	polyprotein [Hepatitis C virus]	34.7	0.92
gi 58198303 gb AAW65859.1	envelope protein [synthetic construct	34.7	0.93
gi 33336957 gb AAQ13146.1	polyprotein [Hepatitis C virus]	34.7	0.95
gi 7649243 gb AAF65811.1	polyprotein precursor [Hepatitis C vir	34.7	0.96
gi 109259770 gb AAW65880.2	envelope protein [synthetic construc	34.7	0.98
gi 64501431 gb AYY41683.1	envelope [Hepatitis C virus]	34.7	0.98
gi 33336563 gb AAQ12949.1	polyprotein [Hepatitis C virus]	34.7	0.99
gi 7649239 gb AAF65809.1	polyprotein precursor [Hepatitis C vir	34.7	0.99
gi 7649247 gb AAF65813.1	polyprotein precursor [Hepatitis C vir	34.7	1.0

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gi 94317855 gb ABF15187.1	polyprotein precursor [Hepatitis C virus]	34.7	1.0
gi 7670903 gb AAF66271.1	polyprotein precursor [Hepatitis C virus]	34.7	1.0
gi 64501443 gb AAY41689.1	envelope [Hepatitis C virus]	34.7	1.0
gi 33336997 gb AAQ13166.1	polyprotein [Hepatitis C virus] >g...	34.7	1.0
gi 7649237 gb AAF65808.1	polyprotein precursor [Hepatitis C virus]	34.7	1.0
gi 33336507 gb AAQ12921.1	polyprotein [Hepatitis C virus]	34.7	1.0
gi 4469530 gb AAD21304.1	polyprotein [Hepatitis C virus]	34.7	1.1
gi 50235322 gb AAT69968.1	polyprotein [Hepatitis C virus]	34.7	1.1
gi 33637202 gb AAQ23757.1	polyprotein [Hepatitis C virus]	34.7	1.1
gi 7649233 gb AAF65806.1	polyprotein precursor [Hepatitis C virus]	34.7	1.1
gi 33637208 gb AAQ23760.1	polyprotein [Hepatitis C virus]	34.7	1.1
gi 7670911 gb AAF66275.1	polyprotein precursor [Hepatitis C virus]	34.7	1.1
gi 7670863 gb AAF66251.1	polyprotein precursor [Hepatitis C virus]	34.7	1.1
gi 53801865 gb AAU94105.1	polyprotein [Hepatitis C virus]	34.7	1.1
gi 13448285 gb AAK26966.1	polyprotein [Hepatitis C virus]	34.7	1.1
gi 7649235 gb AAF65807.1	polyprotein precursor [Hepatitis C virus]	34.7	1.1
gi 4927576 gb AAD33153.1	polyprotein [Hepatitis C virus]	34.7	1.1
gi 33336831 gb AAQ13083.1	polyprotein [Hepatitis C virus]	34.7	1.1
gi 33336779 gb AAQ13057.1	polyprotein [Hepatitis C virus]	34.7	1.1
gi 33336661 gb AAQ12998.1	polyprotein [Hepatitis C virus]	34.7	1.1
gi 13448354 gb AAK27000.1	polyprotein [Hepatitis C virus]	34.7	1.2
gi 84380361 gb ABC58410.1	polyprotein [Hepatitis C virus]	34.7	1.2
gi 37957197 gb AAP03928.1	polyprotein [Hepatitis C virus]	34.3	1.2
gi 5918965 gb AAD56198.1	polyprotein [Hepatitis C virus]	34.3	1.2
gi 90658415 gb ABD97104.1	polyprotein [Hepatitis C virus]	34.3	1.2
gi 13448290 gb AAK26968.1	polyprotein [Hepatitis C virus]	34.3	1.2
gi 33336593 gb AAQ12964.1	polyprotein [Hepatitis C virus]	34.3	1.2
gi 33637190 gb AAQ23751.1	polyprotein [Hepatitis C virus]	34.3	1.2
gi 13448352 gb AAK26999.1	polyprotein [Hepatitis C virus]	34.3	1.2
gi 13448287 gb AAK26967.1	polyprotein [Hepatitis C virus]	34.3	1.2
gi 33336539 gb AAQ12937.1	polyprotein [Hepatitis C virus] >g...	34.3	1.2
gi 33337031 gb AAQ13183.1	polyprotein [Hepatitis C virus]	34.3	1.2
gi 33336801 gb AAQ13068.1	polyprotein [Hepatitis C virus] >g...	34.3	1.2
gi 7649251 gb AAF65815.1	polyprotein precursor [Hepatitis C virus]	34.3	1.2
gi 37957131 gb AAP03895.1	polyprotein [Hepatitis C virus]	34.3	1.3
gi 56342211 dbj BAD73983.1	polyprotein [Hepatitis C virus type]	34.3	1.3
gi 33336659 gb AAQ12997.1	polyprotein [Hepatitis C virus]	34.3	1.3
gi 7649249 gb AAF65814.1	polyprotein precursor [Hepatitis C virus]	34.3	1.3
gi 33336725 gb AAQ13030.1	polyprotein [Hepatitis C virus] >g...	34.3	1.3
gi 33336535 gb AAQ12935.1	polyprotein [Hepatitis C virus] >g...	34.3	1.3
gi 13448283 gb AAK26965.1	polyprotein [Hepatitis C virus]	34.3	1.3
gi 33336973 gb AAQ13154.1	polyprotein [Hepatitis C virus]	34.3	1.3
gi 58220848 gb AAW68051.1	envelope protein [synthetic construct]	34.3	1.3
gi 33336543 gb AAQ12939.1	polyprotein [Hepatitis C virus]	34.3	1.3
gi 62554071 dbj BAD95611.1	polyprotein [Hepatitis C virus]	34.3	1.3
gi 33637198 gb AAQ23755.1	polyprotein [Hepatitis C virus]	34.3	1.3
gi 33336877 gb AAQ13106.1	polyprotein [Hepatitis C virus]	34.3	1.4
gi 33336983 gb AAQ13159.1	polyprotein [Hepatitis C virus]	34.3	1.4
gi 13448464 gb AAK27144.1	polyprotein [Hepatitis C virus]	34.3	1.4
gi 13344957 gb AAK19132.1	polyprotein precursor [Hepatitis C virus]	34.3	1.4
gi 7670915 gb AAF66277.1	polyprotein precursor [Hepatitis C virus]	34.3	1.4
gi 33336663 gb AAQ12999.1	polyprotein [Hepatitis C virus]	34.3	1.4
gi 33336929 gb AAQ13132.1	polyprotein [Hepatitis C virus]	34.3	1.4
gi 33637206 gb AAQ23759.1	polyprotein [Hepatitis C virus]	34.3	1.4
gi 7670913 gb AAF66276.1	polyprotein precursor [Hepatitis C virus]	34.3	1.4
gi 7650256 gb AAF65959.1	polyprotein [Hepatitis C virus]	34.3	1.4
gi 84380358 gb ABC58409.1	polyprotein [Hepatitis C virus] >g...	34.3	1.4
gi 59474 emb CAA37292.1	unnamed protein product [Hepatitis C virus]	34.3	1.5
gi 4927628 gb AAD33205.1	polyprotein [Hepatitis C virus]	34.3	1.5
gi 4927605 gb AAD33182.1	polyprotein [Hepatitis C virus]	34.3	1.5
gi 4927572 gb AAD33149.1	polyprotein [Hepatitis C virus]	34.3	1.5

gi 33637212 gb AAQ23762.1	polyprotein [Hepatitis C virus]	34.3	1.5
gi 33336529 gb AAQ12932.1	polyprotein [Hepatitis C virus]	34.3	1.5
gi 16518682 gb AAL24942.1	glycoprotein [Hepatitis C virus] >...	34.3	1.5
gi 20340011 gb AAM19658.1	E1/E2 protein [Hepatitis C virus]	34.3	1.5
gi 4469527 gb AAD21301.1	polyprotein [Hepatitis C virus]	34.3	1.5
gi 33336945 gb AAQ13140.1	polyprotein [Hepatitis C virus]	34.3	1.5
gi 13448234 gb AAK26941.1	polyprotein [Hepatitis C virus]	34.3	1.5
gi 22129793 ref NP_671491.1	polyprotein [Hepatitis C virus] ...	34.3	1.5
gi 4927597 gb AAD33174.1	polyprotein [Hepatitis C virus]	33.9	1.5
gi 33336781 gb AAQ13058.1	polyprotein [Hepatitis C virus]	33.9	1.6
gi 33336511 gb AAQ12923.1	polyprotein [Hepatitis C virus]	33.9	1.6
gi 33336481 gb AAQ12908.1	polyprotein [Hepatitis C virus]	33.9	1.6
gi 7670929 gb AAF66284.1	polyprotein precursor [Hepatitis C vir	33.9	1.6
gi 13448266 gb AAK26957.1	polyprotein [Hepatitis C virus]	33.9	1.6
gi 33336755 gb AAQ13045.1	polyprotein [Hepatitis C virus] >g...	33.9	1.6
gi 23955759 gb AAN40611.1	polyprotein [Hepatitis C virus]	33.9	1.6
gi 13344961 gb AAK19134.1	polyprotein precursor [Hepatitis C vi	33.9	1.6
gi 4469528 gb AAD21302.1	polyprotein [Hepatitis C virus]	33.9	1.7
gi 13448232 gb AAK26940.1	polyprotein [Hepatitis C virus] >g...	33.9	1.7
gi 13448226 gb AAK26937.1	polyprotein [Hepatitis C virus]	33.9	1.7
gi 4927608 gb AAD33185.1	polyprotein [Hepatitis C virus]	33.9	1.7
gi 4927622 gb AAD33199.1	polyprotein [Hepatitis C virus] >gi...	33.9	1.7
gi 4927568 gb AAD33145.1	polyprotein [Hepatitis C virus]	33.9	1.7
gi 20340013 gb AAM19659.1	E1/E2 protein [Hepatitis C virus]	33.9	1.7
gi 221512 dbj BAA00705.1	structural protein [Hepatitis C virus]	33.9	1.7
gi 33336795 gb AAQ13065.1	polyprotein [Hepatitis C virus]	33.9	1.7
gi 33336763 gb AAQ13049.1	polyprotein [Hepatitis C virus]	33.9	1.7
gi 13448454 gb AAK27049.1	polyprotein [Hepatitis C virus]	33.9	1.7
gi 53801722 gb AAU94034.1	polyprotein [Hepatitis C virus]	33.9	1.7
gi 6521009 dbj BAA88057.1	polyprotein [Hepatitis C virus] (is...	33.9	1.7
gi 33637210 gb AAQ23761.1	polyprotein [Hepatitis C virus]	33.9	1.7
gi 13448478 gb AAK27061.1	polyprotein [Hepatitis C virus]	33.9	1.7
gi 4927632 gb AAD33209.1	polyprotein [Hepatitis C virus] >gi...	33.9	1.7
gi 13448292 gb AAK26969.1	polyprotein [Hepatitis C virus]	33.9	1.7
gi 13448224 gb AAK26936.1	polyprotein [Hepatitis C virus]	33.9	1.7
gi 20340017 gb AAM19661.1	E1/E2 protein [Hepatitis C virus] ...	33.9	1.7
gi 1372958 gb AAB02127.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 30025530 gb AAP04379.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 4927629 gb AAD33206.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 4927609 gb AAD33186.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 4927631 gb AAD33208.1	polyprotein [Hepatitis C virus] >gi...	33.9	1.8
gi 4927580 gb AAD33157.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 33336509 gb AAQ12922.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 22385223 gb AAM96142.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 13448330 gb AAK26988.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 13448260 gb AAK26954.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 4469529 gb AAD21303.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 33336731 gb AAQ13033.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 23955751 gb AAN40607.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 23955749 gb AAN40606.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 33336749 gb AAQ13042.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 33336717 gb AAQ13026.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 13448220 gb AAK26934.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 4927611 gb AAD33188.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 4927604 gb AAD33181.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 4927600 gb AAD33177.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 4927595 gb AAD33172.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 4927620 gb AAD33197.1	polyprotein [Hepatitis C virus]	33.9	1.8
gi 33336645 gb AAQ12990.1	polyprotein [Hepatitis C virus]	33.9	1.9
gi 33637200 gb AAQ23756.1	polyprotein [Hepatitis C virus]	33.9	1.9
gi 29647945 gb AAQ087872.1	polyprotein [Hepatitis C virus]	33.9	1.9

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gi 13448228 gb AAK26938.1	polyprotein [Hepatitis C virus]	33.9	1.9
gi 13448222 gb AAK26935.1	polyprotein [Hepatitis C virus]	33.9	1.9
gi 4927633 gb AAD33210.1	polyprotein [Hepatitis C virus]	33.9	1.9
gi 4927615 gb AAD33192.1	polyprotein [Hepatitis C virus]	33.9	1.9
gi 4927585 gb AAD33162.1	polyprotein [Hepatitis C virus] >gi...	33.9	1.9
gi 436992 gb AAA45602.1	putative	33.9	1.9
gi 37957253 gb AAP03955.1	polyprotein [Hepatitis C virus]	33.9	1.9
gi 33637196 gb AAQ23754.1	polyprotein [Hepatitis C virus]	33.9	1.9
gi 16518644 gb AAL24923.1	glycoprotein [Hepatitis C virus]	33.9	1.9
gi 13448447 gb AAK27046.1	polyprotein [Hepatitis C virus]	33.9	1.9
gi 13448332 gb AAK26989.1	polyprotein [Hepatitis C virus]	33.9	1.9
gi 67810875 gb AYY82024.1	polyprotein [Hepatitis C virus] >g...	33.9	1.9
gi 4469504 gb AAD21278.1	polyprotein [Hepatitis C virus]	33.9	1.9
gi 436990 gb AAA72391.1	[Hepatitis C virus gene, partial cds.],	33.9	1.9
gi 13448328 gb AAK26987.1	polyprotein [Hepatitis C virus]	33.9	1.9
gi 13448312 gb AAK26979.1	polyprotein [Hepatitis C virus]	33.9	2.0
gi 4469514 gb AAD21288.1	polyprotein [Hepatitis C virus]	33.9	2.0
gi 20340019 gb AAM19662.1	E1/E2 protein [Hepatitis C virus] ...	33.9	2.0
gi 7670873 gb AAF66256.1	polyprotein precursor [Hepatitis C vir	33.9	2.0
gi 4927606 gb AAD33183.1	polyprotein [Hepatitis C virus]	33.9	2.0
gi 4927603 gb AAD33180.1	polyprotein [Hepatitis C virus] >gi...	33.9	2.0
gi 4469505 gb AAD21279.1	polyprotein [Hepatitis C virus]	33.9	2.0
gi 13448476 gb AAK27060.1	polyprotein [Hepatitis C virus]	33.9	2.0
gi 20339987 gb AAM19646.1	E1/E2 protein [Hepatitis C virus] ...	33.9	2.0
gi 16517602 gb AAL24763.1	polyprotein [Hepatitis C virus]	33.9	2.0
gi 40389093 gb AAR85724.1	E2 [Hepatitis C virus]	33.5	2.0
gi 13344951 gb AAK19129.1	polyprotein precursor [Hepatitis C vi	33.5	2.0
gi 16517673 gb AAL24798.1	polyprotein [Hepatitis C virus]	33.5	2.0
gi 56342217 dbj BAD73986.1	polyprotein [Hepatitis C virus type	33.5	2.0
gi 4927625 gb AAD33202.1	polyprotein [Hepatitis C virus]	33.5	2.0
gi 4927627 gb AAD33204.1	polyprotein [Hepatitis C virus] >gi...	33.5	2.0
gi 4927626 gb AAD33203.1	polyprotein [Hepatitis C virus]	33.5	2.0
gi 37957173 gb AAP03916.1	polyprotein [Hepatitis C virus]	33.5	2.0
gi 33336859 gb AAQ13097.1	polyprotein [Hepatitis C virus]	33.5	2.0
gi 16517620 gb AAL24772.1	polyprotein [Hepatitis C virus]	33.5	2.0
gi 20339983 gb AAM19644.1	E1/E2 protein [Hepatitis C virus] ...	33.5	2.0
gi 46403731 gb AAS92927.1	E1E2 region of HCV polyprotein [sy...	33.5	2.0
gi 7670865 gb AAF66252.1	polyprotein precursor [Hepatitis C vir	33.5	2.1
gi 40389227 gb AAR85791.1	E2 [Hepatitis C virus]	33.5	2.1
gi 40389047 gb AAR85701.1	E2 [Hepatitis C virus]	33.5	2.1
gi 22385227 gb AAM96144.1	polyprotein [Hepatitis C virus]	33.5	2.1
gi 16517628 gb AAL24776.1	polyprotein [Hepatitis C virus]	33.5	2.1
gi 13448300 gb AAK26973.1	polyprotein [Hepatitis C virus]	33.5	2.1
gi 16517616 gb AAL24770.1	polyprotein [Hepatitis C virus]	33.5	2.1
gi 7670925 gb AAF66282.1	polyprotein precursor [Hepatitis C ...	33.5	2.1
gi 40389307 gb AAR85831.1	E2 [Hepatitis C virus]	33.5	2.1
gi 13448324 gb AAK26985.1	polyprotein [Hepatitis C virus]	33.5	2.1
gi 4927618 gb AAD33195.1	polyprotein [Hepatitis C virus]	33.5	2.1
gi 4469515 gb AAD21289.1	polyprotein [Hepatitis C virus]	33.5	2.1
gi 16518642 gb AAL24922.1	glycoprotein [Hepatitis C virus] >...	33.5	2.1
gi 4927567 gb AAD33144.1	polyprotein [Hepatitis C virus]	33.5	2.1
gi 16517608 gb AAL24766.1	polyprotein [Hepatitis C virus]	33.5	2.2
gi 13448302 gb AAK26974.1	polyprotein [Hepatitis C virus]	33.5	2.2
gi 4927624 gb AAD33201.1	polyprotein [Hepatitis C virus]	33.5	2.2
gi 4927612 gb AAD33189.1	polyprotein [Hepatitis C virus]	33.5	2.2
gi 13448460 gb AAK27052.1	polyprotein [Hepatitis C virus]	33.5	2.2
gi 4927602 gb AAD33179.1	polyprotein [Hepatitis C virus]	33.5	2.2
gi 13448464 gb AAK27054.1	polyprotein [Hepatitis C virus]	33.5	2.2
gi 13448437 gb AAK27041.1	polyprotein [Hepatitis C virus]	33.5	2.2
gi 13448456 gb AAK27050.1	polyprotein [Hepatitis C virus] >g...	33.5	2.2
gi 33413931 gb AAP55691.1	polyprotein [Hepatitis C virus]	33.5	2.2

gi 7670869 gb AAF66254.1	polyprotein precursor [Hepatitis C virus]	33.5	2.2
gi 32423840 gb AAP81306.1	polyprotein [Hepatitis C virus]	33.5	2.3
gi 13448358 gb AAK27002.1	polyprotein [Hepatitis C virus]	33.5	2.3
gi 4927601 gb AAD33178.1	polyprotein [Hepatitis C virus]	33.5	2.3
gi 40389325 gb AAR85840.1	E2 [Hepatitis C virus]	33.5	2.3
gi 13448274 gb AAK26961.1	polyprotein [Hepatitis C virus]	33.5	2.3
gi 16517624 gb AAL24774.1	polyprotein [Hepatitis C virus]	33.5	2.3
gi 4927630 gb AAD33207.1	polyprotein [Hepatitis C virus]	33.5	2.3
gi 4927571 gb AAD33148.1	polyprotein [Hepatitis C virus]	33.5	2.3
gi 16517679 gb AAL24801.1	polyprotein [Hepatitis C virus]	33.5	2.3
gi 33336845 gb AAQ13090.1	polyprotein [Hepatitis C virus]	33.5	2.4
gi 13448415 gb AAK27030.1	polyprotein [Hepatitis C virus]	33.5	2.4
gi 13448304 gb AAK26975.1	polyprotein [Hepatitis C virus]	33.5	2.4
gi 67810859 gb AYY82017.1	polyprotein [Hepatitis C virus]	33.5	2.4
gi 13448482 gb AAK27063.1	polyprotein [Hepatitis C virus]	33.5	2.4
gi 13448362 gb AAK27004.1	polyprotein [Hepatitis C virus]	33.5	2.4
gi 22385183 gb AAM96123.1	polyprotein [Hepatitis C virus] >gi...	33.5	2.4
gi 22385238 gb AAM96149.1	polyprotein [Hepatitis C virus]	33.5	2.4
gi 13448547 gb AAK27095.1	polyprotein [Hepatitis C virus]	33.5	2.4
gi 13448484 gb AAK27064.1	polyprotein [Hepatitis C virus]	33.5	2.4
gi 13448468 gb AAK27056.1	polyprotein [Hepatitis C virus]	33.5	2.4
gi 13448445 gb AAK27045.1	polyprotein [Hepatitis C virus]	33.5	2.4
gi 16517376 gb AAL24650.1	polyprotein [Hepatitis C virus]	33.5	2.4
gi 4927582 gb AAD33159.1	polyprotein [Hepatitis C virus]	33.5	2.4
gi 67810864 gb AYY82019.1	polyprotein [Hepatitis C virus]	33.5	2.5
gi 20339989 gb AAM19647.1	E1/E2 protein [Hepatitis C virus]	33.5	2.5
gi 7670907 gb AAF66273.1	polyprotein precursor [Hepatitis C virus]	33.5	2.5
gi 40389211 gb AAR85783.1	E2 [Hepatitis C virus]	33.5	2.5
gi 33637391 gb AAQ23851.1	polyprotein [Hepatitis C virus]	33.5	2.5
gi 53801929 gb AAU94137.1	polyprotein [Hepatitis C virus]	33.5	2.5
gi 40389407 gb AAR85881.1	E2 [Hepatitis C virus]	33.5	2.5
gi 40389299 gb AAR85827.1	E2 [Hepatitis C virus]	33.5	2.5
gi 40389139 gb AAR85747.1	E2 [Hepatitis C virus] >gi 4038913...	33.5	2.5
gi 40389039 gb AAR85697.1	E2 [Hepatitis C virus]	33.5	2.5
gi 33337179 gb AAQ13257.1	polyprotein [Hepatitis C virus]	33.5	2.5
gi 53802164 gb AAU94253.1	polyprotein [Hepatitis C virus]	33.5	2.5
gi 7670875 gb AAF66257.1	polyprotein precursor [Hepatitis C virus]	33.5	2.5
gi 13448470 gb AAK27057.1	polyprotein [Hepatitis C virus]	33.5	2.6
gi 13448466 gb AAK27055.1	polyprotein [Hepatitis C virus]	33.5	2.6
gi 16517630 gb AAL24777.1	polyprotein [Hepatitis C virus]	33.5	2.6
gi 32423844 gb AAP81308.1	polyprotein [Hepatitis C virus] >gi...	33.5	2.6
gi 33337185 gb AAQ13260.1	polyprotein [Hepatitis C virus]	33.5	2.6
gi 53801923 gb AAU94134.1	polyprotein [Hepatitis C virus]	33.5	2.6
gi 33337145 gb AAQ13240.1	polyprotein [Hepatitis C virus]	33.1	2.6
gi 94322859 gb ABF17689.1	polyprotein precursor [Hepatitis C ...]	33.1	2.6
gi 13448433 gb AAK27039.1	polyprotein [Hepatitis C virus]	33.1	2.6
gi 53801921 gb AAU94133.1	polyprotein [Hepatitis C virus]	33.1	2.6
gi 53801909 gb AAU94127.1	polyprotein [Hepatitis C virus]	33.1	2.6
gi 13448506 gb AAK27075.1	polyprotein [Hepatitis C virus]	33.1	2.7
gi 22385185 gb AAM96124.1	polyprotein [Hepatitis C virus]	33.1	2.7
gi 30025526 gb AAP04377.1	polyprotein [Hepatitis C virus]	33.1	2.7
gi 7728551 gb AAF68724.1	polyprotein [Hepatitis C virus]	33.1	2.7
gi 53801724 gb AAU94035.1	polyprotein [Hepatitis C virus]	33.1	2.7
gi 67810868 gb AYY82021.1	polyprotein [Hepatitis C virus]	33.1	2.7
gi 53802168 gb AAU94255.1	polyprotein [Hepatitis C virus] >gi...	33.1	2.7
gi 67810857 gb AYY82016.1	polyprotein [Hepatitis C virus]	33.1	2.7
gi 53802172 gb AAU94257.1	polyprotein [Hepatitis C virus]	33.1	2.7
gi 53802170 gb AAU94256.1	polyprotein [Hepatitis C virus]	33.1	2.7
gi 40389167 gb AAR85761.1	E2 [Hepatitis C virus]	33.1	2.8
gi 33336619 gb AAQ12977.1	polyprotein [Hepatitis C virus]	33.1	2.8
gi 40389389 gb AAR85872.1	E2 [Hepatitis C virus]	33.1	2.8

gi 33336979 gb AAQ13157.1	polyprotein [Hepatitis C virus]	33.1	2.8
gi 40389277 gb AAR85816.1	E2 [Hepatitis C virus] >gi 4038915...	33.1	2.8
gi 13448504 gb AAK27074.1	polyprotein [Hepatitis C virus]	33.1	2.8
gi 20339825 gb AAM19566.1	E1/E2 protein [Hepatitis C virus]	33.1	2.8
gi 20339823 gb AAM19565.1	E1/E2 protein [Hepatitis C virus]	33.1	2.8
gi 13448486 gb AAK27065.1	polyprotein [Hepatitis C virus]	33.1	2.8
gi 53802211 gb AAU94275.1	polyprotein [Hepatitis C virus]	33.1	2.8
gi 93975 pir S24082	envelope protein - hepatitis C virus (fragm	33.1	2.8
gi 33337229 gb AAQ13282.1	polyprotein [Hepatitis C virus]	33.1	2.8
gi 33337163 gb AAQ13249.1	polyprotein [Hepatitis C virus]	33.1	2.8
gi 13448298 gb AAK26972.1	polyprotein [Hepatitis C virus]	33.1	2.9
gi 40389365 gb AAR85860.1	E2 [Hepatitis C virus]	33.1	2.9
gi 33337059 gb AAQ13197.1	polyprotein [Hepatitis C virus]	33.1	2.9
gi 33336485 gb AAQ12910.1	polyprotein [Hepatitis C virus]	33.1	2.9
gi 53801933 gb AAU94139.1	polyprotein [Hepatitis C virus]	33.1	2.9
gi 56406528 gb AAV87613.1	polyprotein [Hepatitis C virus]	33.1	3.0
gi 19569733 gb AAL92158.1	polyprotein [Hepatitis C virus]	33.1	3.0
gi 13448494 gb AAK27069.1	polyprotein [Hepatitis C virus]	33.1	3.0
gi 7649221 gb AAF65800.1	polyprotein precursor [Hepatitis C vir	33.1	3.0
gi 33336515 gb AAQ12925.1	polyprotein [Hepatitis C virus]	33.1	3.0
gi 13448500 gb AAK27072.1	polyprotein [Hepatitis C virus]	33.1	3.0
gi 33336937 gb AAQ13136.1	polyprotein [Hepatitis C virus]	33.1	3.0
gi 16517374 gb AAL24649.1	polyprotein [Hepatitis C virus]	33.1	3.0
gi 40389341 gb AAR85848.1	E2 [Hepatitis C virus] >gi 4038928...	33.1	3.1
gi 40389265 gb AAR85810.1	E2 [Hepatitis C virus]	33.1	3.1
gi 40389353 gb AAR85854.1	E2 [Hepatitis C virus] >gi 4038924...	33.1	3.1
gi 20339821 gb AAM19564.1	E1/E2 protein [Hepatitis C virus]	33.1	3.1
gi 53801939 gb AAU94142.1	polyprotein [Hepatitis C virus]	33.1	3.1
gi 40389415 gb AAR85885.1	E2 [Hepatitis C virus] >gi 4038941...	33.1	3.1
gi 33337167 gb AAQ13251.1	polyprotein [Hepatitis C virus]	33.1	3.1
gi 33337249 gb AAQ13292.1	polyprotein [Hepatitis C virus] >g...	33.1	3.1
gi 13448270 gb AAK26959.1	polyprotein [Hepatitis C virus]	33.1	3.2
gi 13448258 gb AAK26953.1	polyprotein [Hepatitis C virus]	33.1	3.2
gi 37957175 gb AAP03917.1	polyprotein [Hepatitis C virus]	33.1	3.2
gi 13448496 gb AAK27070.1	polyprotein [Hepatitis C virus]	33.1	3.2
gi 13448488 gb AAK27066.1	polyprotein [Hepatitis C virus]	33.1	3.2
gi 20339835 gb AAM19571.1	E1/E2 protein [Hepatitis C virus]	33.1	3.2
gi 40389099 gb AAR85727.1	E2 [Hepatitis C virus]	33.1	3.3
gi 40389079 gb AAR85717.1	E2 [Hepatitis C virus]	33.1	3.3
gi 37957171 gb AAP03915.1	polyprotein [Hepatitis C virus]	33.1	3.3
gi 7649223 gb AAF65801.1	polyprotein precursor [Hepatitis C vir	33.1	3.3
gi 56406416 gb AAV87557.1	polyprotein [Hepatitis C virus]	33.1	3.3
gi 13448276 gb AAK26962.1	polyprotein [Hepatitis C virus]	33.1	3.3
gi 53802162 gb AAU94252.1	polyprotein [Hepatitis C virus]	33.1	3.3
gi 32423860 gb AAP81316.1	polyprotein [Hepatitis C virus]	33.1	3.3
gi 15866624 gb AAL10411.1	polyprotein [Hepatitis C virus]	33.1	3.3
gi 7728977 gb AAF68775.1	polyprotein precursor [Hepatitis C vir	33.1	3.3
gi 52078280 gb AAU25900.1	polyprotein [Hepatitis C virus]	33.1	3.4
gi 4927634 gb AAD33211.1	polyprotein [Hepatitis C virus] >gi...	33.1	3.4
gi 53802150 gb AAU94246.1	polyprotein [Hepatitis C virus]	33.1	3.4
gi 7728973 gb AAF68773.1	polyprotein precursor [Hepatitis C vir	32.7	3.4
gi 25900865 dbj BAC41270.1	polyprotein [Hepatitis C virus]	32.7	3.4
gi 7728555 gb AAF68726.1	polyprotein [Hepatitis C virus]	32.7	3.4
gi 7728557 gb AAF68727.1	polyprotein [Hepatitis C virus] >gi...	32.7	3.4
gi 53802154 gb AAU94248.1	polyprotein [Hepatitis C virus]	32.7	3.4
gi 53802152 gb AAU94247.1	polyprotein [Hepatitis C virus]	32.7	3.4
gi 53802146 gb AAU94244.1	polyprotein [Hepatitis C virus]	32.7	3.4
gi 33337231 gb AAQ13283.1	polyprotein [Hepatitis C virus]	32.7	3.5
gi 53802160 gb AAU94251.1	polyprotein [Hepatitis C virus]	32.7	3.5
gi 53802156 gb AAU94249.1	polyprotein [Hepatitis C virus]	32.7	3.5
gi 53802148 gb AAU94245.1	polyprotein [Hepatitis C virus]	32.7	3.5

gi 53801944 gb AAU94144.1	polyprotein [Hepatitis C virus]	32.7	3.5
gi 40389379 gb AAR85867.1	E2 [Hepatitis C virus]	32.7	3.6
gi 40389275 gb AAR85815.1	E2 [Hepatitis C virus]	32.7	3.6
gi 40389261 gb AAR85808.1	E2 [Hepatitis C virus]	32.7	3.6
gi 40389403 gb AAR85879.1	E2 [Hepatitis C virus] >gi 4038922...	32.7	3.6
gi 22385174 gb AAM96119.1	polyprotein [Hepatitis C virus]	32.7	3.6
gi 37957193 gb AAP03926.1	polyprotein [Hepatitis C virus]	32.7	3.6
gi 33337223 gb AAQ13279.1	polyprotein [Hepatitis C virus]	32.7	3.6
gi 13448268 gb AAK26958.1	polyprotein [Hepatitis C virus]	32.7	3.6
gi 33337155 gb AAQ13245.1	polyprotein [Hepatitis C virus]	32.7	3.7
gi 33337129 gb AAQ13232.1	polyprotein [Hepatitis C virus]	32.7	3.7
gi 13448280 gb AAK26964.1	polyprotein [Hepatitis C virus]	32.7	3.7
gi 37957177 gb AAP03918.1	polyprotein [Hepatitis C virus]	32.7	3.7
gi 30025514 gb AAP04371.1	polyprotein [Hepatitis C virus]	32.7	3.7
gi 20339829 gb AAM19568.1	E1/E2 protein [Hepatitis C virus]	32.7	3.7
gi 53802158 gb AAU94250.1	polyprotein [Hepatitis C virus]	32.7	3.7
gi 56406476 gb AAV87587.1	polyprotein [Hepatitis C virus]	32.7	3.7
gi 32423866 gb AAP81319.1	polyprotein [Hepatitis C virus] >g...	32.7	3.7
gi 4927581 gb AAD33158.1	polyprotein [Hepatitis C virus]	32.7	3.7
gi 13448492 gb AAK27068.1	polyprotein [Hepatitis C virus]	32.7	3.8
gi 13448236 gb AAK26942.1	polyprotein [Hepatitis C virus]	32.7	3.8
gi 2580421 dbj BAA23132.1	polyprotein [Hepatitis C virus]	32.7	3.8
gi 7728545 gb AAF68721.1	polyprotein [Hepatitis C virus]	32.7	3.8
gi 13448254 gb AAK26951.1	polyprotein [Hepatitis C virus]	32.7	3.8
gi 13448242 gb AAK26945.1	polyprotein [Hepatitis C virus]	32.7	3.8
gi 33336693 gb AAQ13014.1	polyprotein [Hepatitis C virus]	32.7	3.9
gi 33336685 gb AAQ13010.1	polyprotein [Hepatitis C virus]	32.7	3.9
gi 33336689 gb AAQ13012.1	polyprotein [Hepatitis C virus] >g...	32.7	3.9
gi 33336727 gb AAQ13031.1	polyprotein [Hepatitis C virus] >g...	32.7	3.9
gi 33336597 gb AAQ12966.1	polyprotein [Hepatitis C virus]	32.7	3.9
gi 22385233 gb AAM96147.1	polyprotein [Hepatitis C virus]	32.7	3.9
gi 40389363 gb AAR85859.1	E2 [Hepatitis C virus]	32.7	3.9
gi 40389287 gb AAR85821.1	E2 [Hepatitis C virus]	32.7	3.9
gi 40389209 gb AAR85782.1	E2 [Hepatitis C virus]	32.7	3.9
gi 51862090 gb AAU11697.1	envelope E1/E2 [Hepatitis C virus]...	32.7	3.9
gi 33337189 gb AAQ13262.1	polyprotein [Hepatitis C virus]	32.7	4.0

Alignments

> gi|58198305|gb|AAW65860.1| envelope protein [synthetic construct]

Length=577

Score = 41.2 bits (95), Expect = 0.010, Method: Composition-based stats.
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1	GSAARTTSGFVSLFAPGAKQN	21
	GSAARTT+G VSLF+PGAKQN	
Sbjct 221	GSAARTTTGLVSLFSPGAKQN	241

> gi|64501453|gb|AYY41694.1| envelope [Hepatitis C virus]

Length=576

Score = 41.2 bits (95), Expect = 0.011, Method: Composition-based stats.
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21

GSAARTT+G VSLF+PGAKQN
Sbjct 220 GSAARTTTGLVSLFSPGAKQN 240

> gi|58198313|gb|AAW65864.1| envelope protein [synthetic construct]
Length=577

Score = 41.2 bits (95), Expect = 0.011, Method: Composition-based stats.
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G VSLF+PGAKQN
Sbjct 221 GSAARTTTGLVSLFSPGAKQN 241

> gi|58198309|gb|AAW65862.1| envelope protein [synthetic construct]
Length=577

Score = 41.2 bits (95), Expect = 0.011, Method: Composition-based stats.
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G VSLF+PGAKQN
Sbjct 221 GSAARTTTGLVSLFSPGAKQN 241

> gi|64501451|gb|AAY41693.1| envelope [Hepatitis C virus]
Length=576

Score = 41.2 bits (95), Expect = 0.011, Method: Composition-based stats.
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G VSLF+PGAKQN
Sbjct 220 GSAARTTTGLVSLFSPGAKQN 240

> gi|64501435|gb|AAY41685.1| envelope [Hepatitis C virus]
Length=576

Score = 41.2 bits (95), Expect = 0.012, Method: Composition-based stats.
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G VSLF+PGAKQN
Sbjct 220 GSAARTTTGLVSLFSPGAKQN 240

> gi|58198311|gb|AAW65863.1| envelope protein [synthetic construct]
Length=577

Score = 41.2 bits (95), Expect = 0.012, Method: Composition-based stats.
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G VSLF+PGAKQN
Sbjct 221 GSAARTTTGLVSLFSPGAKQN 241

> gi|64501449|gb|AAY41692.1| envelope [Hepatitis C virus]

Length=576

Score = 41.2 bits (95), Expect = 0.012, Method: Composition-based stats.
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G VSLF+PGAKQN
Sbjct 220 GSAARTTTGLVSLFSPGAKQN 240

> gi|64501447|gb|AY41691.1| envelope [Hepatitis C virus]

Length=576

Score = 41.2 bits (95), Expect = 0.012, Method: Composition-based stats.
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G VSLF+PGAKQN
Sbjct 220 GSAARTTTGLVSLFSPGAKQN 240

> gi|2565261|gb|AAC61802.1| E2/NS1 protein [Hepatitis C virus]

Length=364

Score = 39.7 bits (91), Expect = 0.030, Method: Composition-based stats.
Identities = 18/21 (85%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTSG S FAPGAKQN
Sbjct 13 GSAARTTSGITSFFAPGAKQN 33

> gi|15341438|gb|AAK95634.1| polyprotein [Hepatitis C virus]

Length=335

Score = 39.7 bits (91), Expect = 0.031, Method: Composition-based stats.
Identities = 18/21 (85%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT GFV LF+PGAKQN
Sbjct 199 GSAARTTGGFVGLFSPGAKQN 219

> gi|58220842|gb|AAW68049.1| envelope protein [synthetic construct]

Length=607

Score = 39.3 bits (90), Expect = 0.037, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+GF SL +PGAKQN
Sbjct 221 GSAARTTAGFASLLSPGAKQN 241

> gi|64501419|gb|AY41677.1| envelope [Hepatitis C virus]

gi|64501417|gb|AY41676.1| envelope [Hepatitis C virus]

Length=576

Score = 39.3 bits (90), Expect = 0.042, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+GF SL +PGAKQN
Sbjct 220 GSAARTTAGFASLLSPGAKQN 240

> gi|64501423|gb|AY41679.1| envelope [Hepatitis C virus]
Length=576

Score = 39.3 bits (90), Expect = 0.044, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+GF SL +PGAKQN
Sbjct 220 GSAARTTAGFASLLSPGAKQN 240

> gi|64501439|gb|AY41687.1| envelope [Hepatitis C virus]
Length=576

Score = 39.3 bits (90), Expect = 0.044, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAAR T+G VSLF+PGAKQN
Sbjct 220 GSAARITTGLVSLFSPGAKQN 240

> gi|64501427|gb|AY41681.1| envelope [Hepatitis C virus]
Length=576

Score = 39.3 bits (90), Expect = 0.044, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAAR T+G VSLF+PGAKQN
Sbjct 220 GSAARATTGLVSLFSPGAKQN 240

> gi|64501445|gb|AY41690.1| envelope [Hepatitis C virus]
Length=576

Score = 39.3 bits (90), Expect = 0.046, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAAR T+G VSLF+PGAKQN
Sbjct 220 GSAARITTGLVSLFSPGAKQN 240

> gi|13448566|gb|AAK27104.1| polyprotein [Hepatitis C virus]
Length=326

Score = 38.1 bits (87), Expect = 0.099, Method: Composition-based stats.
Identities = 18/21 (85%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTSG VSL +PGAKQN
Sbjct 214 GSAARTTSGLVSLSPGAKQN 234

> gi|58198307|gb|AAW65861.1| envelope protein [synthetic construct]
Length=577

Score = 37.7 bits (86), Expect = 0.13, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART G VSLF+PGAKQN
Sbjct 221 GSAARTMIGLVSLFSPGAKQN 241

> gi|64501455|gb|AYY41695.1| envelope [Hepatitis C virus]
Length=576

Score = 37.7 bits (86), Expect = 0.13, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART G VSLF+PGAKQN
Sbjct 220 GSAARTMIGLVSLFSPGAKQN 240

> gi|64501429|gb|AYY41682.1| envelope [Hepatitis C virus]
Length=576

Score = 37.7 bits (86), Expect = 0.14, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G AAR T+G VSLF+PGAKQN
Sbjct 220 GGAARATTGLVSLFSPGAKQN 240

> gi|33337015|gb|AAQ13175.1| polyprotein [Hepatitis C virus]
Length=115

Score = 37.0 bits (84), Expect = 0.20, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SGF SLF PGAKQN
Sbjct 83 GSAGRTVSGFASLFTPGAKQN 103

> gi|64501425|gb|AYY41680.1| truncated envelope [Hepatitis C virus]
gi|64501421|gb|AYY41678.1| truncated envelope [Hepatitis C virus]
Length=249

Score = 37.0 bits (84), Expect = 0.20, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+GF SL +PGAKQN
Sbjct 220 GSAARTTAGFASLLSPGAKQN 240

> gi|53801738|gb|AAU94042.1| polyprotein [Hepatitis C virus]
gi|53801736|gb|AAU94041.1| polyprotein [Hepatitis C virus]
Length=426

Score = 37.0 bits (84), Expect = 0.21, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+AAR+TSGF+SLF PG+KQ+
Sbjct 199 GTAARSTSGFISLFQPGSKQD 219

> gi|16518692|gb|AAL24947.1| glycoprotein [Hepatitis C virus]
Length=85

Score = 37.0 bits (84), Expect = 0.23, Method: Composition-based stats.
Identities = 19/21 (90%), Positives = 21/21 (100%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+GFVSLF+PGAKQN
Sbjct 55 GSAARTTTGFVSLFSPGAKQN 75

> gi|13448510|gb|AAK27077.1| polyprotein [Hepatitis C virus]
Length=326

Score = 37.0 bits (84), Expect = 0.23, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTSG+V+LF PGAKQ+
Sbjct 214 GSAARTTSGWVNLFNPGAKQD 234

> gi|33337023|gb|AAQ13179.1| polyprotein [Hepatitis C virus]
Length=115

Score = 36.6 bits (83), Expect = 0.24, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SGF SLF PGAKQN
Sbjct 83 GSAGRTVSGFASLFTPAGAKQN 103

> gi|53801728|gb|AAU94037.1| polyprotein [Hepatitis C virus]
Length=426

Score = 36.6 bits (83), Expect = 0.25, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+AAR+TSGF+SLF PG+KQ+
Sbjct 199 GTAARSTSGFISLFQPGSKQD 219

> gi|13448516|gb|AAK27080.1| polyprotein [Hepatitis C virus]
Length=326

Score = 36.6 bits (83), Expect = 0.25, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21

GSAARTTSG+V+LF PGAKQ+
Sbjct 214 GSAARTTSGWVNLFPNGAKQD 234

> gi|130455|sp|P26664|POLG_HCV1 Genome polyprotein [Contains: Core protein p21 (Caps: C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
gi|329874|gb|AAA45676.1| HCV-1
Length=3011

Score = 36.6 bits (83), Expect = 0.26, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA T SGFVSL APGAKQN
Sbjct 390 GSAGHTVSGFVSLLAPGAKQN 410

> gi|67810851|gb|AYY82013.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 36.6 bits (83), Expect = 0.26, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA+TT+G SLF+PGAKQN
Sbjct 390 GSAAKTTAGLTSFLSPGAKQN 410

> gi|67810849|gb|AYY82012.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 36.6 bits (83), Expect = 0.26, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA+TT+G SLF+PGAKQN
Sbjct 390 GSAAKTTAGLTSFLSPGAKQN 410

> gi|14532249|gb|AAK66556.1| HCV type 1a/1b chimera polyprotein [synthetic construct]
gi|14532247|gb|AAK66555.1| HCV type 1a polyprotein [synthetic construct]
gi|14532245|gb|AAK66554.1| HCV type 1a/1b chimera polyprotein [synthetic construct]
Length=3011

Score = 36.6 bits (83), Expect = 0.26, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA T SGFVSL APGAKQN
Sbjct 390 GSAGHTVSGFVSLLAPGAKQN 410

> gi|14532251|gb|AAK66557.1| HCV type 1a/1b chimera mutant polyprotein [synthetic cor
Length=3011

Score = 36.6 bits (83), Expect = 0.26, Method: Composition-based stats.
 Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSA T SGFVSL APGAKQN
 Sbjct 390 GSAGHTVSGFVSSLAPGAKQN 410

> gi|53801732|gb|AAU94039.1| polyprotein [Hepatitis C virus]
 Length=426

Score = 36.6 bits (83), Expect = 0.27, Method: Composition-based stats.
 Identities = 15/21 (71%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 G+AAR+TSGF+SLF PG+KQ+
 Sbjct 199 GTAARSTSGFISLFQPGSKQD 219

> gi|33337057|gb|AAQ13196.1| polyprotein [Hepatitis C virus]
 gi|33337055|gb|AAQ13195.1| polyprotein [Hepatitis C virus]
 gi|33337053|gb|AAQ13194.1| polyprotein [Hepatitis C virus]
 gi|33337051|gb|AAQ13193.1| polyprotein [Hepatitis C virus]
 gi|33337049|gb|AAQ13192.1| polyprotein [Hepatitis C virus]
 gi|33337047|gb|AAQ13191.1| polyprotein [Hepatitis C virus]
 gi|33337043|gb|AAQ13189.1| polyprotein [Hepatitis C virus]
 gi|33337041|gb|AAQ13188.1| polyprotein [Hepatitis C virus]
 gi|33337039|gb|AAQ13187.1| polyprotein [Hepatitis C virus]
 gi|33337037|gb|AAQ13186.1| polyprotein [Hepatitis C virus]
 gi|33337035|gb|AAQ13185.1| polyprotein [Hepatitis C virus]
 gi|33337029|gb|AAQ13182.1| polyprotein [Hepatitis C virus]
 gi|33337027|gb|AAQ13181.1| polyprotein [Hepatitis C virus]
 gi|33337019|gb|AAQ13177.1| polyprotein [Hepatitis C virus]
 gi|33337013|gb|AAQ13174.1| polyprotein [Hepatitis C virus]
 gi|33337011|gb|AAQ13173.1| polyprotein [Hepatitis C virus]
 gi|33337009|gb|AAQ13172.1| polyprotein [Hepatitis C virus]
 gi|33337007|gb|AAQ13171.1| polyprotein [Hepatitis C virus]
 gi|33337003|gb|AAQ13169.1| polyprotein [Hepatitis C virus]
 gi|33336999|gb|AAQ13167.1| polyprotein [Hepatitis C virus]

Length=115

Score = 36.6 bits (83), Expect = 0.28, Method: Composition-based stats.
 Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSA RT SGF SLF PGAKQN
 Sbjct 83 GSAGRTVSGFASLFTPAGAKQN 103

> gi|37957242|gb|AAP03950.1| polyprotein [Hepatitis C virus]
 Length=115

Score = 36.6 bits (83), Expect = 0.28, Method: Composition-based stats.
 Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSA T SGFVSL APGAKQN
 Sbjct 83 GSAGHTVSGFVSSLAPGAKQN 103

> gi|436988|gb|AAA45601.1| putative
Length=138

Score = 36.6 bits (83), Expect = 0.28, Method: Composition-based stats.
Identities = 18/21 (85%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSAA TTSGFVS F+PGAKQN
Sbjct 22 GSAAHTTSGFVSFFSPGAKQN 42

> gi|7649227|gb|AAF65803.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 36.6 bits (83), Expect = 0.30, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSAART +GF SLF+PGAKQN
Sbjct 73 GSAARTAAGFASLFSPGAKQN 93

> gi|37957231|gb|AAP03945.1| polyprotein [Hepatitis C virus]
Length=115

Score = 36.2 bits (82), Expect = 0.32, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSA T SGFVSL APGAKQN
Sbjct 83 GSAGHTVSGFVSLLAPGAKQN 103

> gi|33337017|gb|AAQ13176.1| polyprotein [Hepatitis C virus]
Length=115

Score = 36.2 bits (82), Expect = 0.32, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSA RT SGF SLF PGAKQN
Sbjct 83 GSAGRTVSGFASLFTPAGAKQN 103

> gi|33337005|gb|AAQ13170.1| polyprotein [Hepatitis C virus]
Length=115

Score = 36.2 bits (82), Expect = 0.32, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSA RT SGF SLF PGAKQN
Sbjct 83 GSAGRTVSGFASLFPAGAKQN 103

> gi|67810855|gb|AAY82015.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 36.2 bits (82), Expect = 0.32, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G LF+PGAKQN
Sbjct 390 GSAARTTAGLTGLFSPGAKQN 410

> gi|67810853|gb|AAV82014.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 36.2 bits (82), Expect = 0.32, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G LF+PGAKQN
Sbjct 390 GSAARTTAGLTGLFSPGAKQN 410

> gi|13448514|gb|AAK27079.1| polyprotein [Hepatitis C virus]
Length=326

Score = 36.2 bits (82), Expect = 0.33, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTSG+V+LF PGAKQ+
Sbjct 214 GSAARTTSGWVNLFNPGAKQD 234

> gi|7670859|gb|AAF66249.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 36.2 bits (82), Expect = 0.34, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTSG V LF PGA+QN
Sbjct 73 GSAARTTSGLVGLFNPGAQQN 93

> gi|33336981|gb|AAQ13158.1| polyprotein [Hepatitis C virus]
Length=115

Score = 36.2 bits (82), Expect = 0.34, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SGF SLF PGAKQN
Sbjct 83 GSAGRTVSGFASLFTPAGAKQN 103

> gi|4469531|gb|AAD21305.1| polyprotein [Hepatitis C virus]
Length=326

Score = 36.2 bits (82), Expect = 0.34, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAAR TSGF +LF+PGAKQ+
Sbjct 214 GSAARATSGFANLFSPGAKQD 234

> gi|33337045|gb|AAQ13190.1| polyprotein [Hepatitis C virus]
Length=115

Score = 36.2 bits (82), Expect = 0.36, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SGF SLF PGAKQN
Sbjct 83 GSAGRTVSGFASLFTPAGAKQN 103

> gi|13448244|gb|AAK26946.1| polyprotein [Hepatitis C virus]
Length=326

Score = 36.2 bits (82), Expect = 0.36, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA+TT+GFVSL +PG KQN
Sbjct 214 GSAAKTTAGFVSLLSPGPKQN 234

> gi|33337025|gb|AAQ13180.1| polyprotein [Hepatitis C virus]
Length=115

Score = 36.2 bits (82), Expect = 0.36, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SGF SLF PGAKQN
Sbjct 83 GSAGRTVSGFASLFTPAGAKQN 103

> gi|33337021|gb|AAQ13178.1| polyprotein [Hepatitis C virus]
Length=115

Score = 36.2 bits (82), Expect = 0.36, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SGF SLF PGAKQN
Sbjct 83 GSAGRTVSGFASLFTPAGAKQN 103

> gi|33336921|gb|AAQ13128.1| polyprotein [Hepatitis C virus]
Length=115

Score = 36.2 bits (82), Expect = 0.36, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SGF SLF PGAKQN
Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|53802198|gb|AAU94270.1| polyprotein [Hepatitis C virus]
Length=426

Score = 36.2 bits (82), Expect = 0.38, Method: Composition-based stats.

Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAAR+ SG S+FAPGAKQN
Sbjct 199 GSAARSISGLTSIFAPGAKQN 219

> gi|13448555|gb|AAK27099.1| polyprotein [Hepatitis C virus]

Length=326

Score = 36.2 bits (82), Expect = 0.39, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART SG VSL +PGAKQN
Sbjct 214 GSAARTASGLVSSLSPGAKQN 234

> gi|33336927|gb|AAQ13131.1| polyprotein [Hepatitis C virus]

Length=115

Score = 36.2 bits (82), Expect = 0.39, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGAKQN
Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|37957251|gb|AAP03954.1| polyprotein [Hepatitis C virus]

Length=115

Score = 36.2 bits (82), Expect = 0.40, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA T SGFVSL APGAKQN
Sbjct 83 GSAGHTVSGFVSLLAPGAKQN 103

> gi|37957229|gb|AAP03944.1| polyprotein [Hepatitis C virus]

Length=115

Score = 36.2 bits (82), Expect = 0.40, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA T SGFVSL APGAKQN
Sbjct 83 GSAGHTVSGFVSLLAPGAKQN 103

> gi|33336925|gb|AAQ13130.1| polyprotein [Hepatitis C virus]

gi|33336923|gb|AAQ13129.1| polyprotein [Hepatitis C virus]
gi|33336919|gb|AAQ13127.1| polyprotein [Hepatitis C virus]
gi|33336917|gb|AAQ13126.1| polyprotein [Hepatitis C virus]
gi|33336915|gb|AAQ13125.1| polyprotein [Hepatitis C virus]
gi|33336913|gb|AAQ13124.1| polyprotein [Hepatitis C virus]
gi|33336911|gb|AAQ13123.1| polyprotein [Hepatitis C virus]
gi|33336907|gb|AAQ13121.1| polyprotein [Hepatitis C virus]
gi|33336905|gb|AAQ13120.1| polyprotein [Hepatitis C virus]

gi|33336903|gb|AAQ13119.1| polyprotein [Hepatitis C virus]
gi|33336901|gb|AAQ13118.1| polyprotein [Hepatitis C virus]
gi|33336899|gb|AAQ13117.1| polyprotein [Hepatitis C virus]
gi|33336897|gb|AAQ13116.1| polyprotein [Hepatitis C virus]
gi|33336895|gb|AAQ13115.1| polyprotein [Hepatitis C virus]
gi|33336893|gb|AAQ13114.1| polyprotein [Hepatitis C virus]
gi|33336891|gb|AAQ13113.1| polyprotein [Hepatitis C virus]
gi|33336883|gb|AAQ13109.1| polyprotein [Hepatitis C virus]
gi|33336879|gb|AAQ13107.1| polyprotein [Hepatitis C virus]
gi|33336875|gb|AAQ13105.1| polyprotein [Hepatitis C virus]
gi|33336873|gb|AAQ13104.1| polyprotein [Hepatitis C virus]
gi|33336869|gb|AAQ13102.1| polyprotein [Hepatitis C virus]

Length=115

Score = 36.2 bits (82), Expect = 0.40, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGAKQN
Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|33336495|gb|AAQ12915.1| polyprotein [Hepatitis C virus]

Length=115

Score = 36.2 bits (82), Expect = 0.40, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG VSL APGAKQN
Sbjct 83 GSAGRTVSGLVSLAPGAKQN 103

> gi|33337001|gb|AAQ13168.1| polyprotein [Hepatitis C virus]

Length=115

Score = 35.8 bits (81), Expect = 0.40, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SGF SLF PGAKQN
Sbjct 83 GSAGRTASGFASLFTPAGAKQN 103

> gi|13344963|gb|AAK19135.1| polyprotein precursor [Hepatitis C virus]

Length=415

Score = 35.8 bits (81), Expect = 0.41, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SGF SLF PGAKQN
Sbjct 390 GSAGRTVSGFASLFTPAGAKQN 410

> gi|7670871|gb|AAF66255.1| polyprotein precursor [Hepatitis C virus]

Length=186

Score = 35.8 bits (81), Expect = 0.41, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTSG V LF PGA+QN
Sbjct 73 GSAARTTSGLVGLFNPGAAQNN 93

> gi|53802217|gb|AAU94278.1| polyprotein [Hepatitis C virus]
Length=426

Score = 35.8 bits (81), Expect = 0.41, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAAR+ SG S+FAPGAKQN
Sbjct 199 GSAARSISGLTSIFAPGAKQN 219

> gi|33336881|gb|AAQ13108.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.8 bits (81), Expect = 0.41, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGAKQN
Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|37957244|gb|AAP03951.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.8 bits (81), Expect = 0.41, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA T SGFVSL APGAKQN
Sbjct 83 GSAGHTVSGFVSLLAPGAKQN 103

> gi|37957239|gb|AAP03949.1| polyprotein [Hepatitis C virus]
gi|37957237|gb|AAP03948.1| polyprotein [Hepatitis C virus]
gi|37957235|gb|AAP03947.1| polyprotein [Hepatitis C virus]
gi|37957227|gb|AAP03943.1| polyprotein [Hepatitis C virus]
gi|37957225|gb|AAP03942.1| polyprotein [Hepatitis C virus]
gi|37957223|gb|AAP03941.1| polyprotein [Hepatitis C virus]
gi|37957221|gb|AAP03940.1| polyprotein [Hepatitis C virus]
gi|37957219|gb|AAP03939.1| polyprotein [Hepatitis C virus]
gi|37957217|gb|AAP03938.1| polyprotein [Hepatitis C virus]
gi|37957215|gb|AAP03937.1| polyprotein [Hepatitis C virus]
gi|37957213|gb|AAP03936.1| polyprotein [Hepatitis C virus]
gi|37957211|gb|AAP03935.1| polyprotein [Hepatitis C virus]
gi|37957209|gb|AAP03934.1| polyprotein [Hepatitis C virus]
gi|37957207|gb|AAP03933.1| polyprotein [Hepatitis C virus]
gi|37957205|gb|AAP03932.1| polyprotein [Hepatitis C virus]
gi|37957203|gb|AAP03931.1| polyprotein [Hepatitis C virus]
gi|37957201|gb|AAP03930.1| polyprotein [Hepatitis C virus]
gi|37957199|gb|AAP03929.1| polyprotein [Hepatitis C virus]
gi|37957195|gb|AAP03927.1| polyprotein [Hepatitis C virus]

Length=115

Score = 35.8 bits (81), Expect = 0.42, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA T SGFVSL APGAKQN
Sbjct 83 GSAGHTVSGFVSLLAPGAKQN 103

> gi|33336889|gb|AAQ13112.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.8 bits (81), Expect = 0.42, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGAKQN
Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|13448238|gb|AAK26943.1| polyprotein [Hepatitis C virus]
Length=326

Score = 35.8 bits (81), Expect = 0.42, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA+TT+GFVSL +PG KQN
Sbjct 214 GSAAKTTAGFVSSLSPGPKQN 234

> gi|7670919|gb|AAF66279.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 35.8 bits (81), Expect = 0.42, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTSG V LF PGA+QN
Sbjct 73 GSAARTTSGLVGLFNPGQQN 93

> gi|7670867|gb|AAF66253.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 35.8 bits (81), Expect = 0.42, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTSG V LF PGA+QN
Sbjct 73 GSAARTTSGLVGLFNPGQQN 93

> gi|33336867|gb|AAQ13101.1| polyprotein [Hepatitis C virus]
gi|33336803|gb|AAQ13069.1| polyprotein [Hepatitis C virus]
gi|33336791|gb|AAQ13063.1| polyprotein [Hepatitis C virus]
gi|33336777|gb|AAQ13056.1| polyprotein [Hepatitis C virus]
gi|33336775|gb|AAQ13055.1| polyprotein [Hepatitis C virus]
gi|33336771|gb|AAQ13053.1| polyprotein [Hepatitis C virus]
gi|33336769|gb|AAQ13052.1| polyprotein [Hepatitis C virus]
gi|33336767|gb|AAQ13051.1| polyprotein [Hepatitis C virus]

gi|33336765|gb|AAQ13050.1| polyprotein [Hepatitis C virus]
gi|33336757|gb|AAQ13046.1| polyprotein [Hepatitis C virus]
gi|33336751|gb|AAQ13043.1| polyprotein [Hepatitis C virus]
gi|33336747|gb|AAQ13041.1| polyprotein [Hepatitis C virus]

Length=115

Score = 35.8 bits (81), Expect = 0.43, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGAKQN
Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|33336885|gb|AAQ13110.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.8 bits (81), Expect = 0.44, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGAKQN
Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|16518684|gb|AAL24943.1| glycoprotein [Hepatitis C virus]
Length=85

Score = 35.8 bits (81), Expect = 0.44, Method: Composition-based stats.
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G VSLF+PGAKQN
Sbjct 55 GSAARTTGLVSLFSPGAKQN 75

> gi|7670861|gb|AAF66250.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 35.8 bits (81), Expect = 0.44, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTSG V LF PGA+QN
Sbjct 73 GSAARTTSGLVGLFNPGQQN 93

> gi|7670939|gb|AAF66289.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 35.8 bits (81), Expect = 0.45, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTSG V LF PGA+QN
Sbjct 73 GSAARTTSGLVGLFNPGQQN 93

> gi|33336909|gb|AAQ13122.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.8 bits (81), Expect = 0.47, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGAKQN
Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|4927491|gb|AAD33137.1| polyprotein [Hepatitis C virus]
Length=175

Score = 35.8 bits (81), Expect = 0.47, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G SLF+PGAKQN
Sbjct 65 GSAARTTAGLASLFSPGAKQN 85

> gi|37957257|gb|AAP03957.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.8 bits (81), Expect = 0.48, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA T SGFVSL APGAKQN
Sbjct 83 GSAGHTVSGFVSLLAPGAKQN 103

> gi|13448474|gb|AAK27059.1| polyprotein [Hepatitis C virus]
Length=326

Score = 35.8 bits (81), Expect = 0.49, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA T+GF LFAPGAKQN
Sbjct 214 GSAAAHATAGFAGLFAPGAKQN 234

> gi|37957255|gb|AAP03956.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.8 bits (81), Expect = 0.50, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA T SGFVSL APGAKQN
Sbjct 83 GSAGHTVSGFVSLLAPGAKQN 103

> gi|13448502|gb|AAK27073.1| polyprotein [Hepatitis C virus]
Length=326

Score = 35.8 bits (81), Expect = 0.50, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21

GSAA T+GF SLF+PGAKQN
Sbjct 214 GSAAHATAGFASLFSPGAKQN 234

> gi|37957179|gb|AAP03919.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.8 bits (81), Expect = 0.50, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSAARTTSG LF PGAKQN
Sbjct 83 GSAARTTSGLAGLFTPAGAKQN 103

> gi|13448524|gb|AAK27084.1| polyprotein [Hepatitis C virus]
Length=326

Score = 35.8 bits (81), Expect = 0.51, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GS ARTTSGF + F PGAKQN
Sbjct 214 GSVAR TTSGFANFFNPGAKQN 234

> gi|37957249|gb|AAP03953.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.8 bits (81), Expect = 0.52, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSA T SGFVSL APGAKQN
Sbjct 83 GSAGHTVSGFVSLLAPGAKQN 103

> gi|37957246|gb|AAP03952.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.8 bits (81), Expect = 0.52, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSA T SGFVSL APGAKQN
Sbjct 83 GSAGHTVSGFVSLLAPGAKQN 103

> gi|33336887|gb|AAQ13111.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.8 bits (81), Expect = 0.52, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSA RT SG SLFAPGAKQN
Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|53801742|gb|AAU94044.1| polyprotein [Hepatitis C virus]

Length=426

Score = 35.8 bits (81), Expect = 0.52, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G AAR+TSGF+SLF PG+KQ+
Sbjct 199 GVAARSTSGFISLFQPGSKQD 219

> gi|4927589|gb|AAD33166.1| polyprotein [Hepatitis C virus]

Length=175

Score = 35.4 bits (80), Expect = 0.55, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART +GF SLF+PGAKQN
Sbjct 65 GSAARTAAGEFASLFSPGAKQN 85

> gi|4927496|gb|AAD33142.1| polyprotein [Hepatitis C virus]

gi|4927495|gb|AAD33141.1| polyprotein [Hepatitis C virus]
gi|4927494|gb|AAD33140.1| polyprotein [Hepatitis C virus]
gi|4927493|gb|AAD33139.1| polyprotein [Hepatitis C virus]
gi|4927492|gb|AAD33138.1| polyprotein [Hepatitis C virus]
gi|4927490|gb|AAD33136.1| polyprotein [Hepatitis C virus]
gi|4927489|gb|AAD33135.1| polyprotein [Hepatitis C virus]
gi|4927488|gb|AAD33134.1| polyprotein [Hepatitis C virus]
gi|4927487|gb|AAD33133.1| polyprotein [Hepatitis C virus]

Length=175

Score = 35.4 bits (80), Expect = 0.55, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G SLF+PGAKQN
Sbjct 65 GSAARTTAGLASLFSPGAKQN 85

> gi|53801730|gb|AAU94038.1| polyprotein [Hepatitis C virus]

Length=426

Score = 35.4 bits (80), Expect = 0.55, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G AAR+TSGF+SLF PG+KQ+
Sbjct 199 GVAARSTSGFISLFQPGSKQD 219

> gi|51558189|gb|AAU06654.1| envelope glycoprotein [Hepatitis C virus]

Length=126

Score = 35.4 bits (80), Expect = 0.56, Method: Composition-based stats.
Identities = 18/21 (85%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+AARTTSGF SLF PGAKQN
Sbjct 9 GAAARTTSGFTSLFRPGAKQN 29

> gi|53801726|gb|AAU94036.1| polyprotein [Hepatitis C virus]
Length=426

Score = 35.4 bits (80), Expect = 0.56, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G AAR+TSGF+SLF PG+KQ+
Sbjct 199 GVAARSTSGFISLFQPGSKQD 219

> gi|53801734|gb|AAU94040.1| polyprotein [Hepatitis C virus]
Length=426

Score = 35.4 bits (80), Expect = 0.57, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G AAR+TSGF+SLF PG+KQ+
Sbjct 199 GVAARSTSGFISLFQPGSKQD 219

> gi|33336863|gb|AAQ13099.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.4 bits (80), Expect = 0.57, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGA+QN
Sbjct 83 GSAGRTVSGLASLFAPGARQN 103

> gi|38539525|gb|AAR23635.1| polyprotein [Hepatitis C virus]
Length=184

Score = 35.4 bits (80), Expect = 0.58, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA+TT+G VSLF PGAKQN
Sbjct 68 GSAAQTTAGLVSLFKPGAKQN 88

> gi|221688|dbj|BAA14118.1| X protein [Hepatitis C virus]
Length=129

Score = 35.4 bits (80), Expect = 0.58, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA T SGFVSL APGAKQN
Sbjct 72 GSAGHTVSGFVSSLAPGAKQN 92

> gi|37957233|gb|AAP03946.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.4 bits (80), Expect = 0.59, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA T SGFVSL APGAKQN
Sbjct 83 GSAGHTVSGFVSLLAPGAKQN 103

> gi|53801718|gb|AAU94032.1| polyprotein [Hepatitis C virus]
Length=426

Score = 35.4 bits (80), Expect = 0.59, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G AAR+TSGF+SLF PG+KQ+
Sbjct 199 GVAARSTSGFISLFQPGSKQD 219

> gi|33336821|gb|AAQ13078.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.4 bits (80), Expect = 0.59, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA+RT SG SLFAPGA+QN
Sbjct 83 GSASRTVSGLASLFAPGARQN 103

> gi|4927621|gb|AAD33198.1| polyprotein [Hepatitis C virus]
Length=175

Score = 35.4 bits (80), Expect = 0.60, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G SLF+PGAKQN
Sbjct 65 GSAARTTAGLASLFSPGAKQN 85

> gi|4927579|gb|AAD33156.1| polyprotein [Hepatitis C virus]
Length=175

Score = 35.4 bits (80), Expect = 0.63, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G SLF+PGAKQN
Sbjct 65 GSAARTTAGLASLFSPGAKQN 85

> gi|33336839|gb|AAQ13087.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.4 bits (80), Expect = 0.64, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGA+QN

Sbjct 83 GSAGRTVSGLASLFA[P]GARQN 103

> gi|7670905|gb|AAF66272.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 35.4 bits (80), Expect = 0.64, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTSG V LF PGA+QN
Sbjct 73 GSAARTTSGLVGLFNPGAQQN 93

> gi|13448551|gb|AAK27097.1| polyprotein [Hepatitis C virus]
Length=326

Score = 35.4 bits (80), Expect = 0.66, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GS ARTTSGF + F PGAKQN
Sbjct 214 GSIARTTSGFANFFDPGAKQN 234

> gi|13344959|gb|AAK19133.1| polyprotein precursor [Hepatitis C virus]
Length=415

Score = 35.4 bits (80), Expect = 0.66, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGAKQN
Sbjct 390 GSAGRTVSGLASLFA[P]GARQN 410

> gi|33336865|gb|AAQ13100.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.4 bits (80), Expect = 0.66, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGA+QN
Sbjct 83 GSAGRTVSGLASLFA[P]GARQN 103

> gi|16518694|gb|AAL24948.1| glycoprotein [Hepatitis C virus]
gi|16518690|gb|AAL24946.1| glycoprotein [Hepatitis C virus]
gi|16518688|gb|AAL24945.1| glycoprotein [Hepatitis C virus]
gi|16518686|gb|AAL24944.1| glycoprotein [Hepatitis C virus]
Length=85

Score = 35.4 bits (80), Expect = 0.67, Method: Composition-based stats.
Identities = 18/21 (85%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G VSLF+PGAKQN
Sbjct 55 GSAARTTTGLVSLFSPGAKQN 75

> gi|13448545|gb|AAK27094.1| polyprotein [Hepatitis C virus]
gi|13448543|gb|AAK27093.1| polyprotein [Hepatitis C virus]
Length=326

Score = 35.4 bits (80), Expect = 0.67, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GS ARTTSGF + F PGAKQN
Sbjct 214 GSIARTTSGFANFFDPGAKQN 234

> gi|13448541|gb|AAK27092.1| polyprotein [Hepatitis C virus]
Length=326

Score = 35.4 bits (80), Expect = 0.67, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GS ARTTSGF + F PGAKQN
Sbjct 214 GSIARTTSGFANFFNPGAKQN 234

> gi|33336851|gb|AAQ13093.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.0 bits (79), Expect = 0.70, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGA+QN
Sbjct 83 GSAGRTVSGLASLFAPGARQN 103

> gi|13448539|gb|AAK27091.1| polyprotein [Hepatitis C virus]
Length=326

Score = 35.0 bits (79), Expect = 0.71, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GS ARTTSGF + F PGAKQN
Sbjct 214 GSIARTTSGFANFFDPGAKQN 234

> gi|33336931|gb|AAQ13133.1| polyprotein [Hepatitis C virus]
gi|33336871|gb|AAQ13103.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.0 bits (79), Expect = 0.71, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGAKQN
Sbjct 83 GSAGRTVSGLASLFAPGAKQN 103

> gi|4927584|gb|AAD33161.1| polyprotein [Hepatitis C virus]
Length=175

Score = 35.0 bits (79), Expect = 0.71, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G SLF+PGAKQN
Sbjct 65 GSAARTTAGLASLFSPGAKQN 85

> gi|4927575|gb|AAD33152.1| polyprotein [Hepatitis C virus]
Length=175

Score = 35.0 bits (79), Expect = 0.71, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTT+G SLF+PGAKQN
Sbjct 65 GSAARTTAGLASLFSPGAKQN 85

> gi|53801809|gb|AAU94077.1| polyprotein [Hepatitis C virus]
Length=426

Score = 35.0 bits (79), Expect = 0.72, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+AAR+T+ FVSL APGA+QN
Sbjct 199 GTAARSTASFVSLLAPGARQN 219

> gi|53801937|gb|AAU94141.1| polyprotein [Hepatitis C virus]
Length=426

Score = 35.0 bits (79), Expect = 0.73, Method: Composition-based stats.
Identities = 15/20 (75%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQ 20
G+AAR T+GFVS F+PGAKQ
Sbjct 199 GTAARDTAGFVSFFSPGAKQ 218

> gi|221587|dbj|BAA01582.1| polyprotein precursor [Hepatitis C virus]
Length=3011

Score = 35.0 bits (79), Expect = 0.76, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G AAR SG VSLF PGAKQN
Sbjct 390 GQAARAMSGLVSLFTPAGAKQN 410

> gi|13448316|gb|AAK26981.1| polyprotein [Hepatitis C virus]
gi|13448310|gb|AAK26978.1| polyprotein [Hepatitis C virus]
gi|13448308|gb|AAK26977.1| polyprotein [Hepatitis C virus]
gi|13448306|gb|AAK26976.1| polyprotein [Hepatitis C virus]
Length=327

Score = 35.0 bits (79), Expect = 0.77, Method: Composition-based stats.

Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+ +RTTSGFV L +PGAKQN
Sbjct 215 GAVSRTTSGFVGLLSPGAKQN 235

> gi|33336823|gb|AAQ13079.1| polyprotein [Hepatitis C virus]

Length=115

Score = 35.0 bits (79), Expect = 0.77, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGA+QN
Sbjct 83 GSAGRTVSGLASLFAPGARQN 103

> gi|13448620|gb|AAK27131.1| polyprotein [Hepatitis C virus]

Length=323

Score = 35.0 bits (79), Expect = 0.77, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTSGFV L PG+KQ+
Sbjct 211 GSAARTTSGFVGLLNPGSKQD 231

> gi|33336861|gb|AAQ13098.1| polyprotein [Hepatitis C virus]

gi|33336857|gb|AAQ13096.1| polyprotein [Hepatitis C virus]
gi|33336855|gb|AAQ13095.1| polyprotein [Hepatitis C virus]
gi|33336853|gb|AAQ13094.1| polyprotein [Hepatitis C virus]
gi|33336849|gb|AAQ13092.1| polyprotein [Hepatitis C virus]
gi|33336847|gb|AAQ13091.1| polyprotein [Hepatitis C virus]
gi|33336843|gb|AAQ13089.1| polyprotein [Hepatitis C virus]
gi|33336841|gb|AAQ13088.1| polyprotein [Hepatitis C virus]
gi|33336837|gb|AAQ13086.1| polyprotein [Hepatitis C virus]
gi|33336835|gb|AAQ13085.1| polyprotein [Hepatitis C virus]
gi|33336833|gb|AAQ13084.1| polyprotein [Hepatitis C virus]
gi|33336829|gb|AAQ13082.1| polyprotein [Hepatitis C virus]
gi|33336827|gb|AAQ13081.1| polyprotein [Hepatitis C virus]
gi|33336825|gb|AAQ13080.1| polyprotein [Hepatitis C virus]
gi|33336813|gb|AAQ13074.1| polyprotein [Hepatitis C virus]
gi|33336811|gb|AAQ13073.1| polyprotein [Hepatitis C virus]
gi|33336809|gb|AAQ13072.1| polyprotein [Hepatitis C virus]
gi|33336807|gb|AAQ13071.1| polyprotein [Hepatitis C virus]

Length=115

Score = 35.0 bits (79), Expect = 0.79, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGA+QN
Sbjct 83 GSAGRTVSGLASLFAPGARQN 103

> gi|53801951|gb|AAU94147.1| polyprotein [Hepatitis C virus]

Length=426

Score = 35.0 bits (79), Expect = 0.79, Method: Composition-based stats.
Identities = 15/20 (75%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQ 20
G+AAR T+GFVS F+PGAKQ
Sbjct 199 GTAARDTAGFVSFFSPGAKQ 218

> gi|13448549|gb|AAK27096.1| polyprotein [Hepatitis C virus]
Length=326

Score = 35.0 bits (79), Expect = 0.80, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GS ARTTSGF + F PGAKQN
Sbjct 214 GSIARTTSGFANFFDPGAKQN 234

> gi|13448320|gb|AAK26983.1| polyprotein [Hepatitis C virus]
Length=327

Score = 35.0 bits (79), Expect = 0.80, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+ +RTTSGFV L +PGAKQN
Sbjct 215 GAVSRTTSGFVGLLSPGAKQN 235

> gi|13448588|gb|AAK27115.1| polyprotein [Hepatitis C virus]
gi|13448586|gb|AAK27114.1| polyprotein [Hepatitis C virus]
gi|13448584|gb|AAK27113.1| polyprotein [Hepatitis C virus]
gi|13448582|gb|AAK27112.1| polyprotein [Hepatitis C virus]
Length=326

Score = 35.0 bits (79), Expect = 0.81, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA+TT G VSLF PGAKQN
Sbjct 214 GSAAQTTLGLVSLFRPGAKQN 234

> gi|53802206|gb|AAU94273.1| polyprotein [Hepatitis C virus]
Length=426

Score = 35.0 bits (79), Expect = 0.81, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA+ T GF SLF+PGA+QN
Sbjct 199 GSAAKITQGFSSLFSPGARQN 219

> gi|89519415|gb|ABD75829.1| polyprotein [Hepatitis C virus]
Length=3008

Score = 35.0 bits (79), Expect = 0.81, Method: Composition-based stats.
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQ 20
GSAA+TTSG VS+FAPGA Q
Sbjct 390 GSAAQTTSGLVSMFAPGASQ 409

> gi|33336965|gb|AAQ13150.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.0 bits (79), Expect = 0.82, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLF PGAKQN
Sbjct 83 GSAGRTVSGLASLFTPAGAKQN 103

> gi|13448326|gb|AAK26986.1| polyprotein [Hepatitis C virus]
Length=327

Score = 35.0 bits (79), Expect = 0.82, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+ +RTTSGFV L +PGAKQN
Sbjct 215 GAVSRTTSGFVGLLSPGAKQN 235

> gi|33337033|gb|AAQ13184.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.0 bits (79), Expect = 0.83, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT GF SLF PGAKQN
Sbjct 83 GSAGRTVPGFASLFTPAGAKQN 103

> gi|13448314|gb|AAK26980.1| polyprotein [Hepatitis C virus]
Length=327

Score = 35.0 bits (79), Expect = 0.84, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+ +RTTSGFV L +PGAKQN
Sbjct 215 GAVSRTTSGFVGLLSPGAKQN 235

> gi|56406500|gb|AAV87599.1| polyprotein [Hepatitis C virus]
Length=179

Score = 35.0 bits (79), Expect = 0.85, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTSG V +F PGA+QN
Sbjct 62 GSAARTTSGVVGIFTPGAQQN 82

> gi|33336761|gb|AAQ13048.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.0 bits (79), Expect = 0.85, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG V L APGAKQN
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|13448578|gb|AAK27110.1| polyprotein [Hepatitis C virus]
Length=326

Score = 35.0 bits (79), Expect = 0.86, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA+TT G VSLF PGAKQN
Sbjct 214 GSAAQTTLGLVSLFRPGAKQN 234

> gi|33637194|gb|AAQ23753.1| polyprotein [Hepatitis C virus]
Length=190

Score = 35.0 bits (79), Expect = 0.86, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA R+T+GF LF+PGAKQN
Sbjct 73 GSAGRSTAGFADLFSPGAKQN 93

> gi|33336525|gb|AAQ12930.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.0 bits (79), Expect = 0.87, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG V L APGAKQN
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|13448322|gb|AAK26984.1| polyprotein [Hepatitis C virus]
Length=327

Score = 35.0 bits (79), Expect = 0.87, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+ +RTTSGFV L +PGAKQN
Sbjct 215 GAVSRTTSGFVGLLSPGAKQN 235

> gi|33336639|gb|AAQ12987.1| polyprotein [Hepatitis C virus]
Length=115

Score = 35.0 bits (79), Expect = 0.89, Method: Composition-based stats.

Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGAKQN
Sbjct 83 GSAGRTVSGLAGLFAPGAKQN 103

> gi|13448318|gb|AAK26982.1| polyprotein [Hepatitis C virus]

Length=327

Score = 35.0 bits (79), Expect = 0.89, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+ +RTTSGFV L +PGAKQN
Sbjct 215 GAVSRTTSGFVGLLSPGAKQN 235

> gi|53801935|gb|AAU94140.1| polyprotein [Hepatitis C virus]

Length=426

Score = 35.0 bits (79), Expect = 0.89, Method: Composition-based stats.
Identities = 15/20 (75%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQ 20
G+AAR T+GFVS F+PGAKQ
Sbjct 199 GTAARDTAGFVSFFSPGAKQ 218

> gi|33336815|gb|AAQ13075.1| polyprotein [Hepatitis C virus]

Length=115

Score = 35.0 bits (79), Expect = 0.89, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGA+QN
Sbjct 83 GSAGRTVSGLASLFAPGARQN 103

> gi|7649241|gb|AAF65810.1| polyprotein precursor [Hepatitis C virus]

Length=186

Score = 34.7 bits (78), Expect = 0.90, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART +G SLF+PGAKQN
Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|109259768|gb|AAW65879.2| envelope protein [synthetic construct]

Length=578

Score = 34.7 bits (78), Expect = 0.90, Method: Composition-based stats.
Identities = 14/21 (66%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+A R T+GF LF PGAKQN
Sbjct 221 GTAGRATAGFTELFTPAGAKQN 241

> gi|13448296|gb|AAK26971.1| polyprotein [Hepatitis C virus]
Length=327

Score = 34.7 bits (78), Expect = 0.91, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G A+RTTSG SL APGAKQN
Sbjct 215 GVASRTTSGLASLLAPGAKQN 235

> gi|13448294|gb|AAK26970.1| polyprotein [Hepatitis C virus]
Length=327

Score = 34.7 bits (78), Expect = 0.91, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G A+RTTSG SL APGAKQN
Sbjct 215 GVASRTTSGLASLLAPGAKQN 235

> gi|53801948|gb|AAU94146.1| polyprotein [Hepatitis C virus]
Length=426

Score = 34.7 bits (78), Expect = 0.91, Method: Composition-based stats.
Identities = 15/20 (75%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQ 20
G+AAR T+GFVS F+PGAKQ
Sbjct 199 GTAARDTAGFVSFFSPGAKQ 218

> gi|26053623|ref|NP_751921.1| G E2 protein; viral envelope protein [Hepatitis C virus]
Length=363

Score = 34.7 bits (78), Expect = 0.91, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RTT+G V L PGAKQN
Sbjct 7 GSAGRRTAGLVGLLTPGAKQN 27

> gi|13448580|gb|AAK27111.1| polyprotein [Hepatitis C virus]
Length=326

Score = 34.7 bits (78), Expect = 0.92, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA+TT G VSLF PGAKQN
Sbjct 214 GSAAQTTLGLVSLFRPGAKQN 234

> gi|64501433|gb|AAY41684.1| envelope [Hepatitis C virus]
Length=576

Score = 34.7 bits (78), Expect = 0.92, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAAR T+G SL +PGAKQN
Sbjct 220 GSAARITAGIASLLSPGAKQN 240

> gi|37957282|gb|AAP03969.1| polyprotein [Hepatitis C virus]
Length=115

Score = 34.7 bits (78), Expect = 0.92, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GS ARTT+G SLF PGAKQN
Sbjct 83 GSVARTTAGLTSLFTPAGAKQN 103

> gi|58198303|gb|AAW65859.1| envelope protein [synthetic construct]
Length=577

Score = 34.7 bits (78), Expect = 0.93, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAAR T+G SL +PGAKQN
Sbjct 221 GSAARITAGIASLLSPGAKQN 241

> gi|33336957|gb|AAQ13146.1| polyprotein [Hepatitis C virus]
Length=115

Score = 34.7 bits (78), Expect = 0.95, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLF PGAKQN
Sbjct 83 GSAGRTVSGLASLFTPAGAKQN 103

> gi|7649243|gb|AAF65811.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 34.7 bits (78), Expect = 0.96, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART +G SLF+PGAKQN
Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|109259770|gb|AAW65880.2| envelope protein [synthetic construct]
Length=578

Score = 34.7 bits (78), Expect = 0.98, Method: Composition-based stats.
Identities = 14/21 (66%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+A R T+GF LF PGAKQN

Sbjct 221 GTAGRATAGFTELFTPAGAKQN 241

> gi|64501431|gb|AY41683.1| envelope [Hepatitis C virus]
Length=576

Score = 34.7 bits (78), Expect = 0.98, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAAR T+G SL +PGAKQN
Sbjct 220 GSAARITAGIASLLSPGAKQN 240

> gi|33336563|gb|AAQ12949.1| polyprotein [Hepatitis C virus]
Length=115

Score = 34.7 bits (78), Expect = 0.99, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG LFAPGAKQN
Sbjct 83 GSAGRTVSGLAGLFAPGAKQN 103

> gi|7649239|gb|AAF65809.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 34.7 bits (78), Expect = 0.99, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART +G SLF+PGAKQN
Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|7649247|gb|AAF65813.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 34.7 bits (78), Expect = 1.0, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART +G SLF+PGAKQN
Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|94317855|gb|ABF15187.1| polyprotein precursor [Hepatitis C virus]
Length=176

Score = 34.7 bits (78), Expect = 1.0, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G A RTTSG VSLF PG+KQN
Sbjct 68 GQAGRRTSGLVSLFKPGSKQN 88

> gi|7670903|gb|AAF66271.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 34.7 bits (78), Expect = 1.0, Method: Composition-based stats.
 Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSAARTTSG V LF PGA+ N
 Sbjct 73 GSAARTTSGLVGLFNPGAQHN 93

> gi|64501443|gb|AY41689.1| envelope [Hepatitis C virus]
 Length=576

Score = 34.7 bits (78), Expect = 1.0, Method: Composition-based stats.
 Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSAAR T+G SL +PGAKQN
 Sbjct 220 GSAARITAGIASLLSPGAKQN 240

> gi|33336997|gb|AAQ13166.1| polyprotein [Hepatitis C virus]
 gi|33336995|gb|AAQ13165.1| polyprotein [Hepatitis C virus]
 gi|33336993|gb|AAQ13164.1| polyprotein [Hepatitis C virus]
 gi|33336991|gb|AAQ13163.1| polyprotein [Hepatitis C virus]
 gi|33336989|gb|AAQ13162.1| polyprotein [Hepatitis C virus]
 gi|33336987|gb|AAQ13161.1| polyprotein [Hepatitis C virus]
 gi|33336985|gb|AAQ13160.1| polyprotein [Hepatitis C virus]
 gi|33336977|gb|AAQ13156.1| polyprotein [Hepatitis C virus]
 gi|33336975|gb|AAQ13155.1| polyprotein [Hepatitis C virus]
 gi|33336971|gb|AAQ13153.1| polyprotein [Hepatitis C virus]
 gi|33336969|gb|AAQ13152.1| polyprotein [Hepatitis C virus]
 gi|33336967|gb|AAQ13151.1| polyprotein [Hepatitis C virus]
 gi|33336963|gb|AAQ13149.1| polyprotein [Hepatitis C virus]
 gi|33336961|gb|AAQ13148.1| polyprotein [Hepatitis C virus]
 gi|33336959|gb|AAQ13147.1| polyprotein [Hepatitis C virus]
 gi|33336955|gb|AAQ13145.1| polyprotein [Hepatitis C virus]
 gi|33336953|gb|AAQ13144.1| polyprotein [Hepatitis C virus]
 gi|33336951|gb|AAQ13143.1| polyprotein [Hepatitis C virus]
 gi|33336949|gb|AAQ13142.1| polyprotein [Hepatitis C virus]
 gi|33336947|gb|AAQ13141.1| polyprotein [Hepatitis C virus]
 gi|33336943|gb|AAQ13139.1| polyprotein [Hepatitis C virus]
 gi|33336941|gb|AAQ13138.1| polyprotein [Hepatitis C virus]
 gi|33336939|gb|AAQ13137.1| polyprotein [Hepatitis C virus]
 gi|33336935|gb|AAQ13135.1| polyprotein [Hepatitis C virus]
 gi|33336933|gb|AAQ13134.1| polyprotein [Hepatitis C virus]

Length=115

Score = 34.7 bits (78), Expect = 1.0, Method: Composition-based stats.
 Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSA RT SG SLF PGAKQN
 Sbjct 83 GSAGRTVSGLASLFTPAGAKQN 103

> gi|7649237|gb|AAF65808.1| polyprotein precursor [Hepatitis C virus]
 Length=186

Score = 34.7 bits (78), Expect = 1.0, Method: Composition-based stats.
 Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART +G SLF+PGAKQN
Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|33336507|gb|AAQ12921.1| polyprotein [Hepatitis C virus]
Length=115

Score = 34.7 bits (78), Expect = 1.0, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA T SG VSL APGAKQN
Sbjct 83 GSAGHTVSGLVSLAPGAKQN 103

> gi|4469530|gb|AAD21304.1| polyprotein [Hepatitis C virus]
Length=326

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G AAR TSGF +LF+PGAKQ+
Sbjct 214 GGAARATSGFANLFSPGAKQD 234

> gi|50235322|gb|AAT69968.1| polyprotein [Hepatitis C virus]
Length=3011

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.
Identities = 14/21 (66%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA R+T+G V LF+PGA+QN
Sbjct 390 GSAGRSTAGLVGLFSPGARQN 410

> gi|33637202|gb|AAQ23757.1| polyprotein [Hepatitis C virus]
Length=190

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA R+T+GF LF+PGAKQN
Sbjct 73 GSAGRSTAGFADLFSPGAKQN 93

> gi|7649233|gb|AAF65806.1| polyprotein precursor [Hepatitis C virus]
gi|7649231|gb|AAF65805.1| polyprotein precursor [Hepatitis C virus]
gi|7649225|gb|AAF65802.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART +G SLF+PGAKQN

Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|33637208|gb|AAQ23760.1| polyprotein [Hepatitis C virus]
Length=189

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA R+T+GF LF+PGAKQN
Sbjct 73 GSAGRSTAGFADLFSPGAKQN 93

> gi|7670911|gb|AAF66275.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTS V LF PGA+QN
Sbjct 73 GSAARTTSSLVGLFNPGAQQN 93

> gi|7670863|gb|AAF66251.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTS V LF PGA+QN
Sbjct 73 GSAARTTSSLVGLFNPGAQQN 93

> gi|53801865|gb|AAU94105.1| polyprotein [Hepatitis C virus]
Length=426

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA T SG ++FAPGAKQN
Sbjct 199 GSAAHTVSGLATIFAPGAKQN 219

> gi|13448285|gb|AAK26966.1| polyprotein [Hepatitis C virus]
Length=327

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+ +RTTSGF L APGAKQN
Sbjct 215 GAVSRTTSGFAGLLAPGAKQN 235

> gi|7649235|gb|AAF65807.1| polyprotein precursor [Hepatitis C virus]
gi|7649229|gb|AAF65804.1| polyprotein precursor [Hepatitis C virus]

Length=186

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART +G SLF+PGAKQN
Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|4927576|gb|AAD33153.1| polyprotein [Hepatitis C virus]

Length=175

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+AARTT+G SLF+PGAKQN
Sbjct 65 GTAARTTAGLASLFSPGAKQN 85

> gi|33336831|gb|AAQ13083.1| polyprotein [Hepatitis C virus]

Length=115

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGA+QN
Sbjct 83 GSAGRTVSGLASLFAPGARQN 103

> gi|33336779|gb|AAQ13057.1| polyprotein [Hepatitis C virus]

Length=115

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA+ T SG VSL APGAKQN
Sbjct 83 GSASHTVSGLVSLAPGAKQN 103

> gi|33336661|gb|AAQ12998.1| polyprotein [Hepatitis C virus]

Length=115

Score = 34.7 bits (78), Expect = 1.1, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG LFAPGAKQN
Sbjct 83 GSAGRTVSGLAGLFAPGAKQN 103

> gi|13448354|gb|AAK27000.1| polyprotein [Hepatitis C virus]

Length=326

Score = 34.7 bits (78), Expect = 1.2, Method: Composition-based stats.
Identities = 14/21 (66%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G AARTT+ FV +F+PGA+QN
Sbjct 214 GGAARTTNSFVGMFSPGARQN 234

> gi|84380361|gb|ABC58410.1| polyprotein [Hepatitis C virus]
Length=181

Score = 34.7 bits (78), Expect = 1.2, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+AAR TSG VSLF PGAKQ+
Sbjct 146 GTAARATSGLVSLFTPAGAKQD 166

> gi|37957197|gb|AAP03928.1| polyprotein [Hepatitis C virus]
Length=115

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G A T SGFVSL APGAKQN
Sbjct 83 GXAGHTVSGFVSLLAPGAKQN 103

> gi|5918965|gb|AAD56198.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G AARTT G SLF+PGA QN
Sbjct 390 GQAARTTQGLTSLFSPGASQN 410

> gi|90658415|gb|ABD97104.1| polyprotein [Hepatitis C virus]
Length=3021

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+AAR SG VSLF PGAKQN
Sbjct 390 GNAARGASGIVSLFTPAGAKQN 410

> gi|13448290|gb|AAK26968.1| polyprotein [Hepatitis C virus]
Length=327

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+ +RTTSGF L APGAKQN
Sbjct 215 GAVSRTTSGFAGLLAPGAKQN 235

> gi|33336593|gb|AAQ12964.1| polyprotein [Hepatitis C virus]
Length=115

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG LFAPGAKQN
Sbjct 83 GSAGRTVSGLAGLFAPGAKQN 103

> gi|33637190|gb|AAQ23751.1| polyprotein [Hepatitis C virus]
Length=190

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA R+T+GF LF+PGAKQN
Sbjct 73 GSAGRSTAGFADLFSPGAKQN 93

> gi|13448352|gb|AAK26999.1| polyprotein [Hepatitis C virus]
Length=326

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.
Identities = 14/21 (66%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G AARTT+ FV +F+PGA+QN
Sbjct 214 GGAARTTNSFVGMFSPGARQN 234

> gi|13448287|gb|AAK26967.1| polyprotein [Hepatitis C virus]
Length=327

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+ +RTTSGF L APGAKQN
Sbjct 215 GAVSRTTSGFAGLLAPGAKQN 235

> gi|33336539|gb|AAQ12937.1| polyprotein [Hepatitis C virus]
gi|33336537|gb|AAQ12936.1| polyprotein [Hepatitis C virus]
Length=115

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG V L APGAKQN
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|33337031|gb|AAQ13183.1| polyprotein [Hepatitis C virus]
Length=115

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.

Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSA RT SGF SLF P AKQN
 Sbjct 83 GSAGRTVSGFASLFTPDAKQN 103

> gi|33336801|gb|AAQ13068.1| polyprotein [Hepatitis C virus]
 gi|33336797|gb|AAQ13066.1| polyprotein [Hepatitis C virus]
 gi|33336793|gb|AAQ13064.1| polyprotein [Hepatitis C virus]
 gi|33336789|gb|AAQ13062.1| polyprotein [Hepatitis C virus]
 gi|33336787|gb|AAQ13061.1| polyprotein [Hepatitis C virus]
 gi|33336783|gb|AAQ13059.1| polyprotein [Hepatitis C virus]
 gi|33336759|gb|AAQ13047.1| polyprotein [Hepatitis C virus]
 gi|33336753|gb|AAQ13044.1| polyprotein [Hepatitis C virus]
 gi|33336745|gb|AAQ13040.1| polyprotein [Hepatitis C virus]
 gi|33336743|gb|AAQ13039.1| polyprotein [Hepatitis C virus]
 gi|33336741|gb|AAQ13038.1| polyprotein [Hepatitis C virus]
 gi|33336739|gb|AAQ13037.1| polyprotein [Hepatitis C virus]
 gi|33336541|gb|AAQ12938.1| polyprotein [Hepatitis C virus]
 gi|33336527|gb|AAQ12931.1| polyprotein [Hepatitis C virus]
 gi|33336523|gb|AAQ12929.1| polyprotein [Hepatitis C virus]
 gi|33336521|gb|AAQ12928.1| polyprotein [Hepatitis C virus]
 gi|33336519|gb|AAQ12927.1| polyprotein [Hepatitis C virus]
 gi|33336513|gb|AAQ12924.1| polyprotein [Hepatitis C virus]
 gi|33336503|gb|AAQ12919.1| polyprotein [Hepatitis C virus]
 gi|33336499|gb|AAQ12917.1| polyprotein [Hepatitis C virus]
 gi|33336497|gb|AAQ12916.1| polyprotein [Hepatitis C virus]
 gi|33336493|gb|AAQ12914.1| polyprotein [Hepatitis C virus]
 gi|33336491|gb|AAQ12913.1| polyprotein [Hepatitis C virus]
 gi|33336483|gb|AAQ12909.1| polyprotein [Hepatitis C virus]

Length=115

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.
 Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSA RT SG V L APGAKQN
 Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|7649251|gb|AAF65815.1| polyprotein precursor [Hepatitis C virus]
 Length=186

Score = 34.3 bits (77), Expect = 1.2, Method: Composition-based stats.
 Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSAART +G SLF+PGAKQN
 Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|37957131|gb|AAP03895.1| polyprotein [Hepatitis C virus]
 Length=115

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.
 Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 GSAARTT+ FV +F+PGA+QN

Sbjct 83 GSAARTTNSFVGMFSPGARQN 103

> gi|56342211|gb|BAD73983.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+AARTT GF SLF PG QN
Sbjct 390 GAAARTTHGFTSLFTPQPSQN 410

> gi|33336659|gb|AAQ12997.1| polyprotein [Hepatitis C virus]
Length=115

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG LFAPGAKQN
Sbjct 83 GSAGRTVSGLAGLFAPGAKQN 103

> gi|7649249|gb|AAF65814.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART +G SLF+PGAKQN
Sbjct 73 GSAARTAAGLASLFSPGAKQN 93

> gi|33336725|gb|AAQ13030.1| polyprotein [Hepatitis C virus]
gi|33336713|gb|AAQ13024.1| polyprotein [Hepatitis C virus]
gi|33336705|gb|AAQ13020.1| polyprotein [Hepatitis C virus]
gi|33336699|gb|AAQ13017.1| polyprotein [Hepatitis C virus]
gi|33336697|gb|AAQ13016.1| polyprotein [Hepatitis C virus]
gi|33336683|gb|AAQ13009.1| polyprotein [Hepatitis C virus]
gi|33336673|gb|AAQ13004.1| polyprotein [Hepatitis C virus]
gi|33336671|gb|AAQ13003.1| polyprotein [Hepatitis C virus]
gi|33336669|gb|AAQ13002.1| polyprotein [Hepatitis C virus]
gi|33336667|gb|AAQ13001.1| polyprotein [Hepatitis C virus]
gi|33336665|gb|AAQ13000.1| polyprotein [Hepatitis C virus]
gi|33336657|gb|AAQ12996.1| polyprotein [Hepatitis C virus]
gi|33336655|gb|AAQ12995.1| polyprotein [Hepatitis C virus]
gi|33336653|gb|AAQ12994.1| polyprotein [Hepatitis C virus]
gi|33336651|gb|AAQ12993.1| polyprotein [Hepatitis C virus]
gi|33336649|gb|AAQ12992.1| polyprotein [Hepatitis C virus]
gi|33336647|gb|AAQ12991.1| polyprotein [Hepatitis C virus]
gi|33336643|gb|AAQ12989.1| polyprotein [Hepatitis C virus]
gi|33336641|gb|AAQ12988.1| polyprotein [Hepatitis C virus]
gi|33336637|gb|AAQ12986.1| polyprotein [Hepatitis C virus]
gi|33336635|gb|AAQ12985.1| polyprotein [Hepatitis C virus]
gi|33336633|gb|AAQ12984.1| polyprotein [Hepatitis C virus]
gi|33336631|gb|AAQ12983.1| polyprotein [Hepatitis C virus]
gi|33336629|gb|AAQ12982.1| polyprotein [Hepatitis C virus]

gi|33336627|gb|AAQ12981.1| polyprotein [Hepatitis C virus]
gi|33336625|gb|AAQ12980.1| polyprotein [Hepatitis C virus]
gi|33336623|gb|AAQ12979.1| polyprotein [Hepatitis C virus]
gi|33336621|gb|AAQ12978.1| polyprotein [Hepatitis C virus]
gi|33336617|gb|AAQ12976.1| polyprotein [Hepatitis C virus]
gi|33336615|gb|AAQ12975.1| polyprotein [Hepatitis C virus]
gi|33336613|gb|AAQ12974.1| polyprotein [Hepatitis C virus]
gi|33336591|gb|AAQ12963.1| polyprotein [Hepatitis C virus]
gi|33336587|gb|AAQ12961.1| polyprotein [Hepatitis C virus]
gi|33336579|gb|AAQ12957.1| polyprotein [Hepatitis C virus]
gi|33336575|gb|AAQ12955.1| polyprotein [Hepatitis C virus]
gi|33336571|gb|AAQ12953.1| polyprotein [Hepatitis C virus]
gi|33336569|gb|AAQ12952.1| polyprotein [Hepatitis C virus]
gi|33336567|gb|AAQ12951.1| polyprotein [Hepatitis C virus]
gi|33336559|gb|AAQ12947.1| polyprotein [Hepatitis C virus]
gi|33336557|gb|AAQ12946.1| polyprotein [Hepatitis C virus]
gi|33336547|gb|AAQ12941.1| polyprotein [Hepatitis C virus]
gi|33336545|gb|AAQ12940.1| polyprotein [Hepatitis C virus]

Length=115

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.
 Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1	GSAARTTSGFVSLFAPGAKQN	21
	GSA RT SG LFAPGAKQN	
Sbjct 83	GSAGRTVSGLAGLFAPGAKQN	103

> gi|33336535|gb|AAQ12935.1| polyprotein [Hepatitis C virus]
gi|33336517|gb|AAQ12926.1| polyprotein [Hepatitis C virus]
gi|33336505|gb|AAQ12920.1| polyprotein [Hepatitis C virus]

Length=115

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.
 Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1	GSAARTTSGFVSLFAPGAKQN	21
	GSA RT SG V L APGAKQN	
Sbjct 83	GSAGRTVSGLVGLLAPGAKQN	103

> gi|13448283|gb|AAK26965.1| polyprotein [Hepatitis C virus]
 Length=327

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.
 Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1	GSAARTTSGFVSLFAPGAKQN	21
	G+ +RTTSGF L APGAKQN	
Sbjct 215	GAVSRTTSGFAGLLAPGAKQN	235

> gi|33336973|gb|AAQ13154.1| polyprotein [Hepatitis C virus]
 Length=115

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.
 Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1	GSAARTTSGFVSLFAPGAKQN	21
	GSA RT SG SLF PGAKQN	

Sbjct 83 GSAGRTVSGLASLFTPAGAKQN 103

> gi|58220848|gb|AAW68051.1| envelope protein [synthetic construct]
Length=578

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA +TSG SLF+PG KQN
Sbjct 221 GSAYSTSGLASLFSPGPKQN 241

> gi|33336543|gb|AAQ12939.1| polyprotein [Hepatitis C virus]
Length=115

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG V L APGAKQN
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|62554071|gb|BAD95611.1| polyprotein [Hepatitis C virus]
Length=543

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA TTS F SLF+PG +QN
Sbjct 200 GSAAHTTSRFTSLFSPGPQQN 220

> gi|33637198|gb|AAQ23755.1| polyprotein [Hepatitis C virus]
Length=189

Score = 34.3 bits (77), Expect = 1.3, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA R+T+GF LF+PGAKQN
Sbjct 73 GSAGRSTAGFADLFSPGAKQN 93

> gi|33336877|gb|AAQ13106.1| polyprotein [Hepatitis C virus]
Length=115

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SL APGAKQN
Sbjct 83 GSAGRTVSGLASLLAPGAKQN 103

> gi|33336983|gb|AAQ13159.1| polyprotein [Hepatitis C virus]
Length=115

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLF PGAKQN
Sbjct 83 GSAGRTVSGLASLFTPAGAKQN 103

> gi|13448646|gb|AAK27144.1| polyprotein [Hepatitis C virus]
Length=315

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA+TTSG SLF PGAKQ+
Sbjct 210 GSAAQTTSGLASLFNPGAKQD 230

> gi|13344957|gb|AAK19132.1| polyprotein precursor [Hepatitis C virus]
Length=415

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLFAPGA+QN
Sbjct 390 GSAGRTVSGLASLFAPGARQN 410

> gi|7670915|gb|AAF66277.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTS V LF PGA+QN
Sbjct 73 GSAARTTSSLVGLFNPGQQN 93

> gi|33336663|gb|AAQ12999.1| polyprotein [Hepatitis C virus]
Length=115

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG LFAPGAKQN
Sbjct 83 GSAGRTVSGLAGLFAPGAKQN 103

> gi|33336929|gb|AAQ13132.1| polyprotein [Hepatitis C virus]
Length=115

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21

GSA R SG SLFAPGAKQN
Sbjct 83 GSAGRASVGLASFAPGAKQN 103

> gi|33637206|gb|AAQ23759.1| polyprotein [Hepatitis C virus]
Length=189

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA R+T+GF LF+PGAKQN
Sbjct 73 GSAGRSTAGFADLFSPGAKQN 93

> gi|7670913|gb|AAF66276.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTS V LF PGA+QN
Sbjct 73 GSAARTTSSLVGLFNPGAAQQN 93

> gi|7650256|gb|AAF65959.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.
Identities = 15/20 (75%), Positives = 16/20 (80%), Gaps = 0/20 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQ 20
G+ ARTTSGF SLF PGA Q
Sbjct 390 GATARTTSGFTSLFTP GASQ 409

> gi|84380358|gb|ABC58409.1| polyprotein [Hepatitis C virus]
gi|84380351|gb|ABC58406.1| polyprotein [Hepatitis C virus]
Length=181

Score = 34.3 bits (77), Expect = 1.4, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+AAR TSG VSLF PGAKQ+
Sbjct 146 GTAARATSGLVSLFTP GASQ 166

> gi|59474|emb|CAA37292.1| unnamed protein product [Hepatitis C virus]
Length=309

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAAR+T+G SLF PGA+QN
Sbjct 262 GSAARSTAGVASLFTP GARQN 282

> gi|4927628|gb|AAD33205.1| polyprotein [Hepatitis C virus]
Length=175

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART +G SLF+PGAKQN
Sbjct 65 GSAARTAAGLASLFSPGAKQN 85

> gi|4927605|gb|AAD33182.1| polyprotein [Hepatitis C virus]
Length=175

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART +G SLF+PGAKQN
Sbjct 65 GSAARTAAGLASLFSPGAKQN 85

> gi|4927572|gb|AAD33149.1| polyprotein [Hepatitis C virus]
Length=175

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART +G SLF+PGAKQN
Sbjct 65 GSAARTAAGLASLFSPGAKQN 85

> gi|33637212|gb|AAQ23762.1| polyprotein [Hepatitis C virus]
Length=190

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA R+T+GF LF+PGAKQN
Sbjct 73 GSAGRSTAGFADLFSPGAKQN 93

> gi|33336529|gb|AAQ12932.1| polyprotein [Hepatitis C virus]
Length=115

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG V L APGAKQN
Sbjct 83 GSAGRSTVSGLVGLLAPGAKQN 103

> gi|16518682|gb|AAL24942.1| glycoprotein [Hepatitis C virus]
gi|16518680|gb|AAL24941.1| glycoprotein [Hepatitis C virus]
gi|16518678|gb|AAL24940.1| glycoprotein [Hepatitis C virus]
gi|16518676|gb|AAL24939.1| glycoprotein [Hepatitis C virus]
Length=85

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAAR T+G VSLF+PGAKQN
Sbjct 55 GSAARATTGLVSLFSPGAKQN 75

> gi|20340011|gb|AAM19658.1| E1/E2 protein [Hepatitis C virus]
Length=154

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+A+RTT+GF SLF PGA+QN
Sbjct 105 GTASRTTAGFASLFNPGARQN 125

> gi|4469527|gb|AAD21301.1| polyprotein [Hepatitis C virus]
Length=326

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAAR TSG +LF+PGAKQ+
Sbjct 214 GSAARATSGLANLFSPGAKQD 234

> gi|33336945|gb|AAQ13140.1| polyprotein [Hepatitis C virus]
Length=115

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLF PGAKQN
Sbjct 83 GSAGRTVSGLASLFTPAGKQN 103

> gi|13448234|gb|AAK26941.1| polyprotein [Hepatitis C virus]
Length=326

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA+TT+G VSL +PG KQN
Sbjct 214 GSAAKTTAGLVSSLSPGPKQN 234

> gi|22129793|ref|NP_671491.1| G polyprotein [Hepatitis C virus]
gi|2316098|gb|AAB66324.1| G polyprotein [Hepatitis C virus]
Length=3011

Score = 34.3 bits (77), Expect = 1.5, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RTT+G V L PGAQN
Sbjct 390 GSAGRTTAGLVGLTPGAKQN 410

> gi|4927597|gb|AAD33174.1| polyprotein [Hepatitis C virus]
Length=175

Score = 33.9 bits (76), Expect = 1.5, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART +G SLF+PGAKQN
Sbjct 65 GSAARTAAGLASLFSPGAKQN 85

> gi|33336781|gb|AAQ13058.1| polyprotein [Hepatitis C virus]
Length=115

Score = 33.9 bits (76), Expect = 1.6, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG V L APGAKQN
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|33336511|gb|AAQ12923.1| polyprotein [Hepatitis C virus]
Length=115

Score = 33.9 bits (76), Expect = 1.6, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG V L APGAKQN
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|33336481|gb|AAQ12908.1| polyprotein [Hepatitis C virus]
Length=115

Score = 33.9 bits (76), Expect = 1.6, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG V L APGAKQN
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|7670929|gb|AAF66284.1| polyprotein precursor [Hepatitis C virus]
Length=186

Score = 33.9 bits (76), Expect = 1.6, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAARTTSG V LF PGA+ N
Sbjct 73 GSAARTTSGLVGLFNPQAHN 93

> gi|13448266|gb|AAK26957.1| polyprotein [Hepatitis C virus]
Length=326

Score = 33.9 bits (76), Expect = 1.6, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA+TT+G VSL +PG KQN
Sbjct 214 GSAAKTTAGLVSLLSPGPKQN 234

> gi|33336755|gb|AAQ13045.1| polyprotein [Hepatitis C virus]
gi|33336533|gb|AAQ12934.1| polyprotein [Hepatitis C virus]
gi|33336487|gb|AAQ12911.1| polyprotein [Hepatitis C virus]
Length=115

Score = 33.9 bits (76), Expect = 1.6, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA T SG VSL APGAKQN
Sbjct 83 GSAGHTVSGLVSLLAPGAKQN 103

> gi|23955759|gb|AAN40611.1| polyprotein [Hepatitis C virus]
Length=191

Score = 33.9 bits (76), Expect = 1.6, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GS ARTTSGF LF PGA QN
Sbjct 73 GSVARTTSGFTGLFNPGASQN 93

> gi|13344961|gb|AAK19134.1| polyprotein precursor [Hepatitis C virus]
Length=415

Score = 33.9 bits (76), Expect = 1.6, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG SLF PGAKQN
Sbjct 390 GSAGRTVSGLASLFTPAGAKQN 410

> gi|4469528|gb|AAD21302.1| polyprotein [Hepatitis C virus]
Length=326

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAAR TSG +LF+PGAKQ+
Sbjct 214 GSAARATGLANLFSPGAKQD 234

> gi|13448232|gb|AAK26940.1| polyprotein [Hepatitis C virus]
gi|13448230|gb|AAK26939.1| polyprotein [Hepatitis C virus]
Length=326

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA+TT+G VSL +PG KQN
Sbjct 214 GSAAKTTAGLVSSLSPGPQKQN 234

> gi|13448226|gb|AAK26937.1| polyprotein [Hepatitis C virus]
Length=326

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA+TT+G VSL +PG KQN
Sbjct 214 GSAAKTTAGLVSSLSPGPQKQN 234

> gi|4927608|gb|AAD33185.1| polyprotein [Hepatitis C virus]
Length=175

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART +G SLF+PGAKQN
Sbjct 65 GSAARTAAGLASLFSPGAKQN 85

> gi|4927622|gb|AAD33199.1| polyprotein [Hepatitis C virus]
gi|4927598|gb|AAD33175.1| polyprotein [Hepatitis C virus]
Length=175

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART +G SLF+PGAKQN
Sbjct 65 GSAARTAAGLASLFSPGAKQN 85

> gi|4927568|gb|AAD33145.1| polyprotein [Hepatitis C virus]
Length=175

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAART +G SLF+PGAKQN
Sbjct 65 GSAARTAAGLASLFSPGAKQN 85

> gi|20340013|gb|AAM19659.1| E1/E2 protein [Hepatitis C virus]
Length=154

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G+A+RTT+GF SLF PGA+QN
Sbjct 105 GTASRTTAGFASLFNPGARQN 125

> gi|221512|gb|BAA00705.1| structural protein [Hepatitis C virus]
Length=513

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G AAR SG VSLF PGAKQN
Sbjct 390 GQAARAMSGLVSLFTPAGAKQN 410

> gi|33336795|gb|AAQ13065.1| polyprotein [Hepatitis C virus]
Length=115

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG V L APGAKQN
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|33336763|gb|AAQ13049.1| polyprotein [Hepatitis C virus]
Length=115

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.
Identities = 16/21 (76%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSA RT SG V L APGAKQN
Sbjct 83 GSAGRTVSGLVGLLAPGAKQN 103

> gi|13448454|gb|AAK27049.1| polyprotein [Hepatitis C virus]
Length=326

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.
Identities = 15/21 (71%), Positives = 16/21 (76%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
GSAA T+GF LF PGAKQN
Sbjct 214 GSAAAHATAGFAGLFTPAGAKQN 234

> gi|53801722|gb|AAU94034.1| polyprotein [Hepatitis C virus]
Length=426

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.
Identities = 14/21 (66%), Positives = 18/21 (85%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
G AAR+TSGF+ LF PG+KQ+
Sbjct 199 GVAARSTSGFIGLFQPGSKQD 219

> gi|6521009|dbj|BAA88057.1| polyprotein [Hepatitis C virus (isolate VAT96)]
 gi|82007035|sp|Q9QAX1|POLG_HCVVA Genome polyprotein [Contains: Core protein p21 (Caps C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
 Length=3033

Score = 33.9 bits (76), Expect = 1.7, Method: Composition-based stats.
 Identities = 15/21 (71%), Positives = 17/21 (80%), Gaps = 0/21 (0%)

Query 1 GSAARTTSGFVSLFAPGAKQN 21
 G AARTT G VSLF PG++QN
 Sbjct 390 GHAARTTHGLVSLFTPQGSQQN 410

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[Deselect all](#)

[Distance tree of results](#)

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples

Posted date: Jul 21, 2006 3:13 AM
 Number of letters in database: 1,312,719,415
 Number of sequences in database: 3,807,609
 Lambda K H
 0.311 0.123 0.341
 Gapped
 Lambda K H
 0.267 0.0410 0.140
 Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Sequences: 3807609
 Number of Hits to DB: 4479366
 Number of extensions: 36593
 Number of successful extensions: 28
 Number of sequences better than 10: 0
 Number of HSP's better than 10 without gapping: 0
 Number of HSP's gapped: 28
 Number of HSP's successfully gapped: 0
 Length of query: 21
 Length of database: 1312719415
 Length adjustment: 0
 Effective length of query: 21
 Effective length of database: 1312719415
 Effective search space: 27567107715
 Effective search space used: 27567107715
 T: 11
 A: 40
 X1: 16 (7.2 bits)
 X2: 38 (14.6 bits)
 X3: 64 (24.7 bits)
 S1: 42 (20.8 bits)
 S2: 70 (31.6 bits)



results of BLAST

BLASTP 2.2.14 [May-07-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference:

Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

RID: 1153602248-17953-92119523316.BLASTQ4

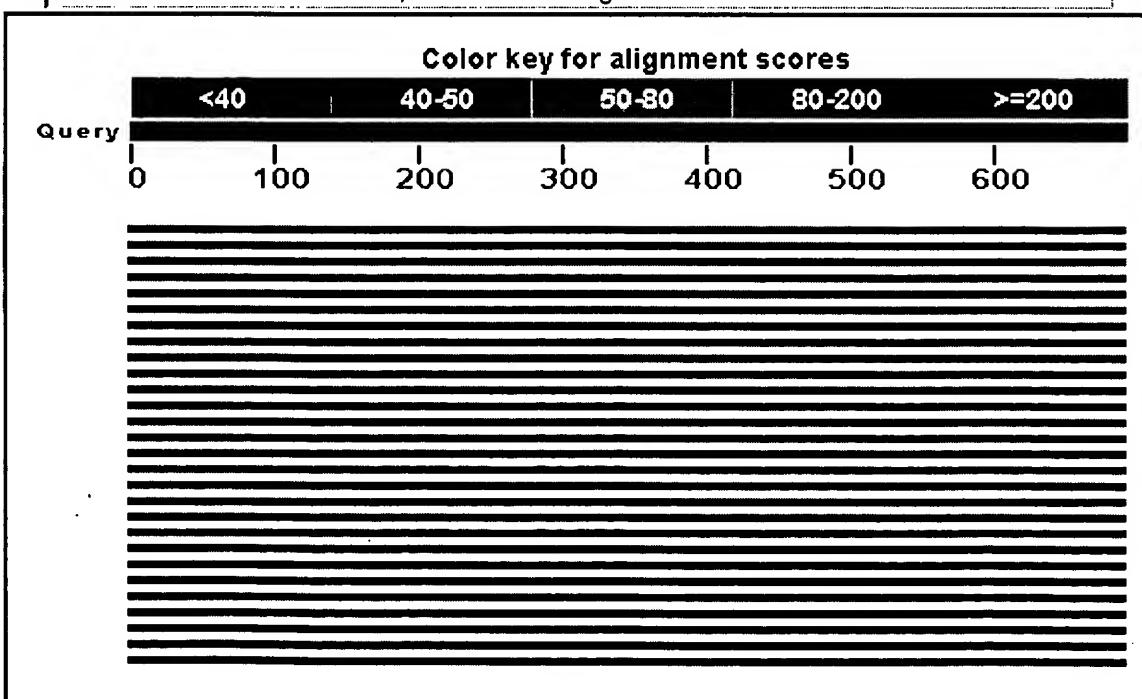
Database: Non-redundant SwissProt sequences
208,958 sequences; 78,544,511 total letters

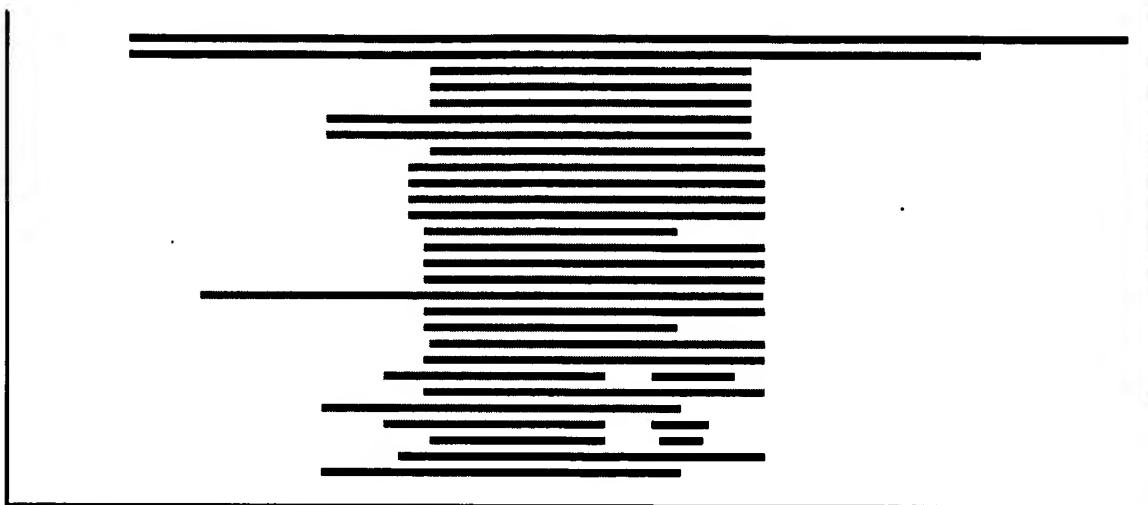
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=685

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Distance tree of results NEW

Sequences producing significant alignments:	Score (Bits)	E Value
gi 130455 sp P26664 POLG_HCV1	Genome polyprotein [Contains: C...]	1302 0.0
gi 130461 sp P27958 POLG_HCVH	Genome polyprotein [Contains: C...]	1268 0.0
gi 130458 sp P26663 POLG_HCVBK	Genome polyprotein [Contains: ...]	1232 0.0
gi 266820 sp Q00269 POLG_HCVJT	Genome polyprotein [Contains: ...]	1229 0.0
gi 81992806 sp Q81754 POLG_HCVH9	Genome polyprotein [Contains...]	1229 0.0
gi 68565847 sp Q9WMX2 POLG_HCVCO	Genome polyprotein [Contains...]	1228 0.0
gi 266821 sp P29846 POLG_HCVTW	Genome polyprotein [Contains: ...]	1226 0.0
gi 130469 sp P26662 POLG_HCVJA	Genome polyprotein [Contains: ...]	1221 0.0
gi 81960062 sp Q913D4 POLG_HCVIN	Genome polyprotein [Contains...]	1207 0.0
gi 81924266 sp O91936 POLG_HCVSA	Genome polyprotein [Contains...]	1150 0.0
gi 81924482 sp O92529 POLG_HCVT5	Genome polyprotein [Contains...]	1146 0.0
gi 81985682 sp Q5I2N3 POLG_HCV6A	Genome polyprotein [Contains...]	1142 0.0
gi 81924483 sp O92530 POLG_HCVVN	Genome polyprotein [Contains...]	1134 0.0
gi 81924484 sp O92531 POLG_HCVVO	Genome polyprotein [Contains...]	1133 0.0
gi 81921386 sp O39929 POLG_HCVED	Genome polyprotein [Contains...]	1130 0.0
gi 81921385 sp O39928 POLG_HCVEV	Genome polyprotein [Contains...]	1127 0.0
gi 81921384 sp O39927 POLG_HCVEU	Genome polyprotein [Contains...]	1122 0.0
gi 81924485 sp O92532 POLG_HCVVP	Genome polyprotein [Contains...]	1121 0.0
gi 81938291 sp Q68798 POLG_HCVJL	Genome polyprotein [Contains...]	1121 0.0
gi 81992783 sp Q81258 POLG_HCVNZ	Genome polyprotein [Contains...]	1084 0.0
gi 75566979 sp Q81495 POLG_HCVK3	Genome polyprotein [Contains...]	1079 0.0
gi 82007035 sp Q9QAX1 POLG_HCVVA	Genome polyprotein [Contains...]	1079 0.0
gi 82004405 sp Q9DHD6 POLG_HCVJP	Genome polyprotein [Contains...]	1073 0.0
gi 130468 sp P26661 POLG_HCVJ8	Genome polyprotein [Contains: ...]	1070 0.0
gi 81992797 sp Q81487 POLG_HCVTR	Genome polyprotein [Contains...]	1065 0.0
gi 130466 sp P26660 POLG_HCVJ6	Genome polyprotein [Contains: ...]	1065 0.0
gi 81938267 sp Q68749 POLG_HCVBB	Genome polyprotein [Contains...]	1064 0.0
gi 81938293 sp Q68801 POLG_HCVJK	Genome polyprotein [Contains...]	1063 0.0
gi 81967359 sp Q99IB8 POLG_HCVJF	Genome polyprotein [Contains...]	1043 0.0
gi 68565638 sp Q69422 POLG_GBVB	Genome polyprotein [Contains:...]	400 1e-110
gi 46396995 sp Q96662 POLG_BVDVC	Genome polyprotein [Contains...]	81.3 1e-14
gi 1346739 sp P19711 POLG_BVDVN	Genome polyprotein [Contains:...]	79.7 3e-14
gi 400808 sp Q01499 POLG_BDVVS	Genome polyprotein [Contains: ...]	79.0 5e-14
gi 130457 sp P21530 POLG_CSFVB	Genome polyprotein [Contains: ...]	75.5 5e-13
gi 14917023 sp P19712 POLG_CSFVA	Genome polyprotein [Contains...]	75.5 6e-13
gi 130522 sp P04517 POLG_TEV	Genome polyprotein [Contains: P1...]	65.1 8e-10
gi 3914417 sp Q84934 POLG_PPVSK	Genome polyprotein [Contains:...]	56.6 3e-07

G

gi 130505 sp P17766 POLG_PPVNA	Genome polyprotein [Contains: ...]	56.2	4e-07	
gi 464430 sp P17767 POLG_PPVRA	Genome polyprotein [Contains: ...]	55.5	6e-07	
gi 6226884 sp P13529 POLG_PPVD	Genome polyprotein [Contains: ...]	55.5	6e-07	
gi 21431801 sp P31999 POLG_LMV0	Genome polyprotein [Contains: ...]	55.1	7e-07	
gi 3914412 sp P89509 POLG_TUMVJ	Genome polyprotein [Contains: ...]	55.1	8e-07	
gi 417510 sp Q01500 POLG_PEMVC	Genome polyprotein [Contains: ...]	55.1	9e-07	
gi 548557 sp Q02597 POLG_TUMVQ	Genome polyprotein [Contains: ...]	54.7	1e-06	
gi 56757564 sp P05769 POLG_MVEV5	Genome polyprotein [Contains: ...]	53.9	2e-06	
gi 21431806 sp P21231 POLG_SBMVN	Genome polyprotein [Contains: ...]	53.5	3e-06	
gi 3914399 sp P89876 POLG_LMVE	Genome polyprotein [Contains: ...]	52.0	8e-06	G
gi 62900634 sp Q6XW15 POLG_BTMV	Genome polyprotein [Contains: ...]	51.6	9e-06	
gi 3914397 sp Q65399 POLG_BCMVN	Genome polyprotein [Contains: ...]	51.6	9e-06	
gi 3914418 sp Q89330 POLG_ZYMR	Genome polyprotein [Contains: ...]	51.2	1e-05	
gi 3914419 sp Q90069 POLG_SBMVG	Genome polyprotein [Contains: ...]	50.4	2e-05	
gi 266813 sp P29990 POLG_DEN26	Genome polyprotein [Contains: ...]	50.4	2e-05	
gi 3915808 sp P18479 POLG_ZYMC	Genome polyprotein [Contains: ...]	50.1	2e-05	
gi 20141657 sp O36979 POLG_ZYMS	Genome polyprotein [Contains: ...]	49.7	4e-05	
gi 68067450 sp P17765 POLG_BYMV	Genome polyprotein [Contains: ...]	49.7	4e-05	
gi 1709704 sp P14340 POLG_DEN2N	Genome polyprotein [Contains: ...]	49.3	5e-05	
gi 130490 sp P27395 POLG_JAEV1	Genome polyprotein [Contains: ...]	49.3	5e-05	
gi 417507 sp P32886 POLG_JAEVJ	Genome polyprotein [Contains: ...]	49.3	5e-05	
gi 266814 sp P29991 POLG_DEN27	Genome polyprotein [Contains: ...]	48.9	6e-05	
gi 130491 sp P19110 POLG_JAEV5	Genome polyprotein [Contains: ...]	48.9	7e-05	
gi 130428 sp P07564 POLG_DEN2J	Genome polyprotein [Contains: ...]	48.5	9e-05	
gi 46396621 sp Q85197 POLG_PVMA	Genome polyprotein [Contains: ...]	48.1	1e-04	
gi 464429 sp P33515 POLG_MCFA	Genome polyprotein [Contains: C...]	48.1	1e-04	
gi 39932633 sp P27914_2	{Segment 2 of 2} Genome polyprotein ...	47.8	1e-04	
gi 130430 sp P12823 POLG_DEN2P	Genome polyprotein [Contains: ...]	47.8	1e-04	
gi 130509 sp P29152 POLG_PSBMV	Genome polyprotein [Contains: ...]	47.4	2e-04	
gi 400818 sp Q02963 POLG_PVYHU	Genome polyprotein [Contains: ...]	46.2	4e-04	G
gi 8247947 sp P09814 POLG_TVMV	Genome polyprotein [Contains: ...]	46.2	4e-04	
gi 3914379 sp Q65730 POLG_BSTV1	Genome polyprotein [Contains: ...]	45.8	4e-04	
gi 41019473 sp P09866 POLG_DEN4	Genome polyprotein [Contains: ...]	45.4	6e-04	
gi 130437 sp P27915 POLG_DEN3	Genome polyprotein [Contains: C...]	45.4	6e-04	
gi 1346743 sp P18247 POLG_PVYN	Genome polyprotein [Contains: ...]	45.1	9e-04	
gi 130530 sp P19901 POLG_YEFV2	Genome polyprotein [Contains: ...]	44.7	0.001	
gi 130529 sp P03314 POLG_YEFV1	Genome polyprotein [Contains: ...]	44.7	0.001	
gi 26006959 sp O60231 DHX16_HUMAN	Putative pre-mRNA-splicing ...	43.1	0.003	G
gi 38502930 sp Q7YR39 DHX16_PANTR	Putative pre-mRNA-splicing ...	43.1	0.003	G
gi 37999909 sp P06935 POLG_WNV	Genome polyprotein [Contains: ...]	43.1	0.004	G
gi 19862987 sp Q10752 CDC28_SCHPO	Putative ATP-dependent RNA hel	42.0	0.007	
gi 464427 sp P33478 POLG_DEN1S	Genome polyprotein [Contains: ...]	41.6	0.010	
gi 6093763 sp O56075 POLG_PEMVM	Genome polyprotein [Contains: ...]	40.4	0.023	
gi 46396755 sp P90245 POL1_BAMMN	Genome polyprotein 1 [Contai...	39.7	0.032	
gi 1709707 sp Q01299 POLG_TBEVH	Genome polyprotein [Contains: ...]	39.7	0.035	
gi 6226885 sp P14336 POLG_TBEVW	Genome polyprotein [Contains: ...]	39.3	0.042	
gi 1709706 sp Q01901 POLG_PRSVH	Genome polyprotein [Contains: ...]	39.3	0.047	
gi 549698 sp P36009 DHR2 YEAST	Probable ATP-dependent RNA hel...	39.3	0.050	G
gi 464428 sp P29837 POLG_LANVT	Genome polyprotein [Contains: ...]	38.9	0.053	
gi 54041622 sp P15043 RECQ_ECOLI	ATP-dependent DNA helicase recQ	38.1	0.11	
gi 22654276 sp O94762 RECQ5_HUMAN	ATP-dependent DNA helicase Q5	37.7	0.13	G
gi 19859341 sp P40724 RECQ_SALTY	ATP-dependent DNA helicase recQ	37.7	0.14	
gi 17366114 sp Q9VGI8 BLM_DROME	Bloom syndrome protein homolo...	37.4	0.16	G
gi 130494 sp P14335 POLG_KUNJM	Genome polyprotein [Contains: ...]	37.4	0.19	
gi 20137928 sp Q9BKQ8 DHX35_CAEEL	Probable ATP-dependent RNA hel	37.0	0.21	G
gi 130520 sp P07720 POLG_TBEVS	Genome polyprotein [Contains: ...]	37.0	0.22	
gi 20137971 sp Q9H5Z1 DHX35_HUMAN	Probable ATP-dependent RNA hel	36.6	0.30	G
gi 21431859 sp P34305 RHA2_CAEEL	Putative ATP-dependent RNA heli	36.6	0.30	G

<u>gi 61212955 sp Q5RBD4 DHX35_PONPY</u>	Probable ATP-dependent RNA helicase	<u>36.2</u>	0.36	
<u>gi 464912 sp P35187 SGS1_YEAST</u>	ATP-dependent helicase SGS1 (Helicase SGS1)	<u>35.0</u>	0.88	G
<u>gi 18202817 sp Q9CL21 RECQL_PASMU</u>	ATP-dependent DNA helicase recQL	<u>35.0</u>	0.98	
<u>gi 2500112 sp P71359 RECQL_HAEIN</u>	ATP-dependent DNA helicase recQL	<u>35.0</u>	0.98	
<u>gi 1705486 sp P54132 BLM_HUMAN</u>	Bloom syndrome protein (RecQL protein)	<u>33.1</u>	3.3	G
<u>gi 5921178 sp O88700 BLM_MOUSE</u>	Bloom syndrome protein homolog (mBLM)	<u>33.1</u>	3.5	G
<u>gi 130804 sp P20095 PRP2_YEAST</u>	Pre-mRNA-splicing factor ATP-dependent	<u>33.1</u>	3.6	G
<u>gi 3915519 sp O45244 DHX16_CAEEL</u>	Probable pre-mRNA-splicing factor	<u>33.1</u>	3.6	G
<u>gi 24212040 sp Q8UDM3 MURE_AGRFT5</u>	UDP-N-acetylmuramoylalanyl-D...	<u>32.7</u>	4.3	G
<u>gi 17366086 sp Q9I920 BLM_CHICK</u>	Bloom syndrome protein homolog	<u>32.0</u>	6.5	G
<u>gi 730353 sp Q04538 POLG_POWVL</u>	Genome polyprotein [Contains: ...]	<u>32.0</u>	7.0	
<u>gi 59803058 sp Q9SEL7 DEGP5_ARATH</u>	Protease Dö-like 5, chloroplast	<u>31.6</u>	8.9	G

Alignments[Get selected sequences](#)[Select all](#)[Deselect all](#)[Distance tree of results](#)

> gi|130455|sp|P26664|POLG_HCV1 Genome polyprotein [Contains: Core protein p21 (Capsid C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirus) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
Length=3011

Score = 1302 bits (3370), Expect = 0.0, Method: Composition-based stats.
Identities = 683/685 (99%), Positives = 683/685 (99%), Gaps = 0/685 (0%)

Query 1	APITAYAQQTGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct 1027	APITAYAQQTGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query 61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct 1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query 121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct 1147	DSRGSLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query 181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct 1207	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query 241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct 1267	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query 301	LGIGTVLDQAETAGARLVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEV	360
Sbjct 1327	LGIGTVLDQAETAGARLVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEV	1386
Query 361	GGRHLIFCHSKKKCDELAALKVALGINAVAYYRGLDVSVIPIGDVVVVATDALMTGYTG	420
Sbjct 1387	GGRHLIFCHSKKKCDELAALKVALGINAVAYYRGLDVSVIPGDVVVVATDALMTGYTG	1446



NCBI

results of BLAST

BLASTP 2.2.14 [May-07-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference:

Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

RID: 1153602163-31376-31136956327.BLASTQ1

Database: pat

301,733 sequences; 55,455,050 total letters

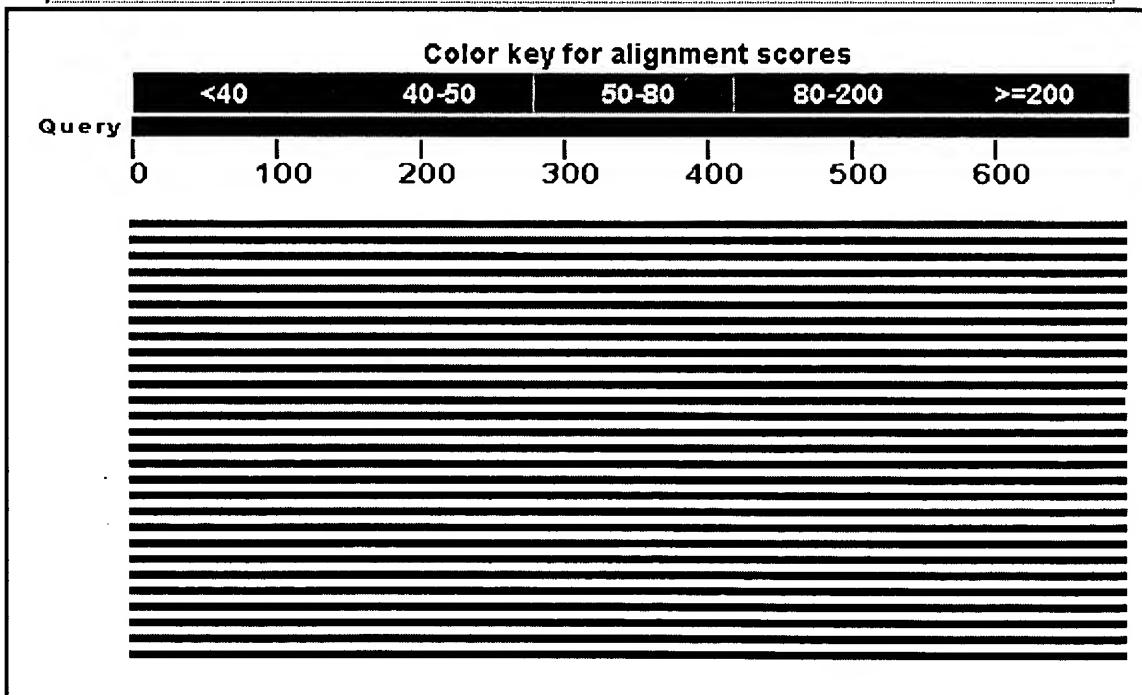
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

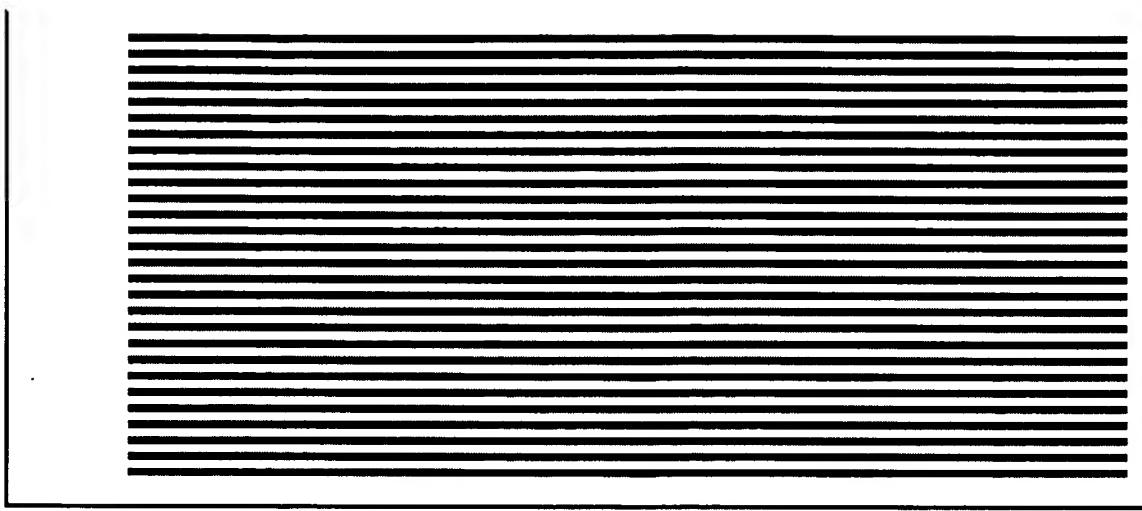
[Taxonomy reports](#)**Query=**

Length=685

Distribution of 102 Blast Hits on the Query Sequence

Mouse-over to show defline and scores, click to show alignments





Distance tree of results NEW

Sequences producing significant alignments:	Score (Bits)	E Value
gi 594200 gb AAA55807.1 Sequence 53 from Patent EP 0318216 >...	1303	0.0
gi 31689077 gb AAP61048.1 Sequence 2 from patent US 6538123 ...	1302	0.0
gi 21508650 gb AAM58139.1 Sequence 1 from patent US 6379886	1302	0.0
gi 593530 gb AAA55137.1 Sequence 2 from Patent EP 0388232	1302	0.0
gi 14101397 gb AAE53714.1 Sequence 66 from patent US 6150087	1301	0.0
gi 14101433 gb AAE53750.1 Sequence 138 from patent US 6150087	1299	0.0
gi 594199 gb AAA55806.1 Sequence 47 from Patent EP 0318216 >...	1299	0.0
gi 14101409 gb AAE53726.1 Sequence 89 from patent US 6150087	1298	0.0
gi 592432 gb AAA54039.1 Sequence 14 from Patent WO 8904669	1297	0.0
gi 14101402 gb AAE53719.1 Sequence 75 from patent US 6150087	1297	0.0
gi 33737406 gb AAQ41059.1 Sequence 23 from patent US 6576417...	1293	0.0
gi 14101391 gb AAE53708.1 Sequence 54 from patent US 6150087	1292	0.0
gi 14101424 gb AAE53741.1 Sequence 124 from patent US 6150087	1290	0.0
gi 91165235 gb ABE25678.1 Sequence 3 from patent US 7022323	1286	0.0
gi 12828946 gb AAE50646.1 Sequence 2 from patent US 6127116	1286	0.0
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gi 75915319 gb ABA29873.1 Sequence 20 from patent US 6921634...	1283	0.0
gi 14103322 gb AAE54756.1 Sequence 5 from patent US 6153421	1283	0.0
gi 12828947 gb AAE50647.1 Sequence 20 from patent US 6127116	1282	0.0
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gi 91135471 gb ABE17566.1 Sequence 7 from patent US 6986892 ...	1261	0.0
gi 56611438 gb AAW04088.1 Sequence 2 from patent US 6790612 ...	1253	0.0
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gi 56611444 gb AAW04094.1 Sequence 9 from patent US 6790612 ...	1251	0.0
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gi 91149570 gb ABE23185.1	Sequence 4 from patent US 7009044	1062	0.0

gi 83327409 gb ABC05586.11	Sequence 13 from patent US 6960431	1062	0.0
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gi 15110181 gb AAE67845.11	Sequence 40 from patent US 6217872...	1049	0.0
gi 17920439 gb AAE86059.11	Sequence 12 from patent US 6312889...	999	0.0
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gi 33759589 gb AAQ52079.11	Sequence 54 from patent US 6593083...	985	0.0
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gi 56627909 gb AAW06245.11	Sequence 4 from patent US 6797809 ...	951	0.0
gi 33759587 gb AAQ52077.11	Sequence 52 from patent US 6593083...	936	0.0
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gi 91135477 gb ABE17572.11	Sequence 19 from patent US 6986892...	900	0.0
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gi 56569104 gb AAV99350.11	Sequence 270 from patent US 676202...	706	0.0
gi 4529953 emb CAA02554.11	unnamed protein product [unidentif...	704	0.0
gi 56569045 gb AAV99291.11	Sequence 200 from patent US 6762024	700	0.0
gi 6088499 emb CAB58629.11	Putative NS3 region PT-NANBH; rest...	565	7e-161
gi 17915387 gb AAE84113.11	Sequence 9 from patent US 6306579 ...	536	4e-152
gi 33759553 gb AAQ52043.11	Sequence 4 from patent US 6593083 ...	531	1e-150
gi 40114189 gb AAR55316.11	Sequence 265 from patent US 661333...	528	9e-150
gi 33759592 gb AAQ52082.11	Sequence 59 from patent US 6593083...	525	1e-148
gi 40160940 gb AAR67292.11	Sequence 1 from patent US 6635257	523	3e-148
gi 17915386 gb AAE84112.11	Sequence 2 from patent US 6306579 ...	520	3e-147
gi 40114191 gb AAR55318.11	Sequence 267 from patent US 661333...	518	9e-147
gi 53920899 gb AAU97762.11	Sequence 36 from patent US 6727092...	516	5e-146
gi 53920898 gb AAU97761.11	Sequence 32 from patent US 6727092...	516	5e-146
gi 40114190 gb AAR55317.11	Sequence 266 from patent US 661333...	516	5e-146
gi 53920895 gb AAU97758.11	Sequence 20 from patent US 6727092...	515	7e-146
gi 53920897 gb AAU97760.11	Sequence 28 from patent US 6727092...	515	7e-146
gi 53920896 gb AAU97759.11	Sequence 25 from patent US 6727092...	515	7e-146
gi 53920900 gb AAU97763.11	Sequence 38 from patent US 6727092...	515	8e-146
gi 53920894 gb AAU97757.11	Sequence 18 from patent US 6727092...	515	9e-146
gi 53920901 gb AAU97764.11	Sequence 40 from patent US 6727092...	514	2e-145
gi 40114199 gb AAR55325.11	Sequence 274 from patent US 661333...	513	3e-145
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gi 40160941 gb AAR67293.11	Sequence 2 from patent US 6635257	511	1e-144
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gi 3211590 gb AAC21350.1 I83293	Sequence 84 from patent US 57...	509	3e-144
gi 42711673 gb AAS35883.11	Sequence 57 from patent US 6689368...	509	4e-144
gi 40114193 gb AAR55320.11	Sequence 269 from patent US 661333...	509	5e-144
gi 40114196 gb AAR55322.11	Sequence 271 from patent US 661333...	509	6e-144
gi 40114200 gb AAR55326.11	Sequence 275 from patent US 661333...	508	1e-143
gi 40114198 gb AAR55324.11	Sequence 273 from patent US 661333...	508	1e-143
gi 21508658 gb AAM58145.11	Sequence 7 from patent US 6379886 ...	507	2e-143
gi 40114201 gb AAR55327.11	Sequence 276 from patent US 661333...	506	4e-143
gi 40114192 gb AAR55319.11	Sequence 268 from patent US 661333...	504	1e-142
gi 40153769 gb AAR65055.11	Sequence 5 from patent US 6630298 ...	488	9e-138
gi 15108286 gb AAE67322.11	Sequence 45 from patent US 6210962...	487	2e-137
gi 15108277 gb AAE67313.11	Sequence 7 from patent US 6210962 ...	484	2e-136
gi 91126695 gb ABE13386.11	Sequence 85 from patent US 6977144	479	4e-135
gi 40114202 gb AAR55328.11	Sequence 277 from patent US 661333...	459	5e-129
gi 40114204 gb AAR55329.11	Sequence 278 from patent US 661333...	457	3e-128
gi 594197 gb AAA55804.11	Sequence 41 from Patent EP 0318216	454	3e-127

gi 14101374 gb AAE53691.1	Sequence 20 from patent US 6150087	451	2e-126
gi 91126693 gb ABE13384.1	Sequence 83 from patent US 6977144	436	5e-122
gi 47268050 gb AAT26677.1	Sequence 394 from patent US 672016...	400	4e-111
gi 3211582 gb AAC21342.1 I83285	Sequence 68 from patent US 57...	392	9e-109
gi 62786768 gb AAY06807.1	Sequence 2 from patent US 6870043	388	2e-107
gi 5997134 gb AAE20681.1	Sequence 15 from patent US 5849532 ...	387	3e-107
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gi 57163355 emb CAI40583.1	unnamed protein product [GB virus C/	384	2e-106
gi 47268062 gb AAT26683.1	Sequence 401 from patent US 672016...	384	2e-106
gi 91126696 gb ABE13387.1	Sequence 86 from patent US 6977144	370	4e-102
gi 47267592 gb AAT26448.1	Sequence 83 from patent US 6720166...	361	2e-99
gi 91126697 gb ABE13388.1	Sequence 87 from patent US 6977144	360	5e-99
gi 47268052 gb AAT26678.1	Sequence 395 from patent US 672016...	357	3e-98
gi 5991332 gb AAE18141.1	Sequence 10 from patent US 5843639 ...	344	2e-94
gi 15108287 gb AAE67323.1	Sequence 46 from patent US 6210962...	339	9e-93
gi 21506997 gb AAM57587.1	Sequence 2 from patent US 6372883 ...	338	2e-92
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gi 56629275 gb AAW06836.1	Sequence 24 from patent US 6800456	323	7e-88
gi 56629260 gb AAW06821.1	Sequence 1 from patent US 6800456	322	9e-88
gi 56629261 gb AAW06822.1	Sequence 3 from patent US 6800456	321	2e-87
gi 91126698 gb ABE13389.1	Sequence 88 from patent US 6977144	318	2e-86
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gi 14480055 gb AAE62017.1	Sequence 1 from patent US 6197536	316	6e-86
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gi 14101377 gb AAE53694.1	Sequence 26 from patent US 6150087	316	7e-86
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gi 56629269 gb AAW06830.1	Sequence 12 from patent US 6800456	308	1e-83
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gi 40194429 gb AAR78470.1	Sequence 53 from patent US 6653127...	298	1e-80
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gi 40194405 gb AAR78446.1	Sequence 4 from patent US 6653127 ...	294	3e-79
gi 40194409 gb AAR78450.1	Sequence 8 from patent US 6653127 ...	293	8e-79
gi 56629274 gb AAW06835.1	Sequence 22 from patent US 6800456	291	3e-78
gi 14480059 gb AAE62021.1	Sequence 5 from patent US 6197536	289	9e-78
gi 40148288 gb AAR63521.1	Sequence 11 from patent US 6623921...	287	3e-77
gi 14480057 gb AAE62019.1	Sequence 3 from patent US 6197536	282	1e-75
gi 91126700 gb ABE13391.1	Sequence 90 from patent US 6977144	280	7e-75
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gi 1248641 emb CAA01932.1	PT-NANBH polyprotein [synthetic const	276	7e-74
gi 14101398 gb AAE53715.1	Sequence 68 from patent US 6150087...	276	7e-74
gi 91126694 gb ABE13385.1	Sequence 84 from patent US 6977144	274	3e-73
gi 14101371 gb AAE53688.1	Sequence 14 from patent US 6150087	273	6e-73
gi 1926565 emb CAA02095.1	partial NANBH-PT polyprotein [Non-A,	272	1e-72
gi 33759585 gb AAQ52075.1	Sequence 49 from patent US 6593083...	269	1e-71
gi 56569058 gb AAV99304.1	Sequence 223 from patent US 676202...	265	2e-70
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gi 47268464 gb AAT26884.1	Sequence 605 from patent US 672016...	246	1e-64
gi 3992552 gb AAC85979.1 AR005496	Sequence 74 from patent US 574	238	2e-62
gi 3211581 gb AAC21341.1 I83284	Sequence 67 from patent US 57...	230	6e-60
gi 3992536 gb AAC85963.1 AR005480	Sequence 58 from patent US 574	229	7e-60
gi 3992540 gb AAC85967.1 AR005484	Sequence 62 from patent US 574	229	1e-59
gi 33759586 gb AAQ52076.1	Sequence 50 from patent US 6593083...	229	1e-59
gi 23316906 gb AAN21401.1	Sequence 1 from patent US 6416946 ...	225	2e-58
gi 5991331 gb AAE18140.1	Sequence 8 from patent US 5843639 >...	223	7e-58
gi 14101382 gb AAE53699.1	Sequence 36 from patent US 6150087	223	9e-58
gi 33759583 gb AAQ52073.1	Sequence 47 from patent US 6593083...	220	4e-57
gi 33759559 gb AAQ52049.1	Sequence 16 from patent US 6593083...	220	6e-57
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gi 42713549 gb AAS36696.1	Sequence 16 from patent US 6692751	201	4e-51
gi 33759580 gb AAQ52070.1	Sequence 44 from patent US 6593083...	200	4e-51
gi 3211584 gb AAC21344.1 I83287	Sequence 72 from patent US 57...	200	7e-51
gi 3992615 gb AAC86042.1 AR005559	Sequence 9 from patent US 5747	199	8e-51
gi 33759579 gb AAQ52069.1	Sequence 43 from patent US 6593083...	197	3e-50
gi 33759577 gb AAQ52067.1	Sequence 41 from patent US 6593083...	194	2e-49
gi 3992551 gb AAC85978.1 AR005495	Sequence 73 from patent US 574	193	8e-49
gi 3992535 gb AAC85962.1 AR005479	Sequence 57 from patent US 574	187	4e-47
gi 28072520 gb AAO30428.1	Sequence 40 from patent US 6322965	186	1e-46
gi 3992539 gb AAC85966.1 AR005483	Sequence 61 from patent US 574	185	2e-46
gi 2486047 gb AAB74183.1 I47801	Sequence 7 from patent US 563959	182	1e-45
gi 56568953 gb AAV99199.1	Sequence 30 from patent US 6762024...	182	2e-45
gi 33759576 gb AAQ52066.1	Sequence 40 from patent US 6593083...	180	7e-45
gi 31689217 gb AAP61069.1	Sequence 94 from patent US 6538126	174	3e-43
gi 23316907 gb AAN21402.1	Sequence 2 from patent US 6416946 ...	173	6e-43
gi 33759575 gb AAQ52065.1	Sequence 39 from patent US 6593083...	165	2e-40
gi 2486052 gb AAB74188.1 I47806	Sequence 12 from patent US 56395	162	1e-39
gi 2486048 gb AAB74184.1 I47802	Sequence 8 from patent US 563959	162	2e-39
gi 3211588 gb AAC21348.1 I83291	Sequence 80 from patent US 57...	161	3e-39
gi 3990878 gb AAC84305.1 AR000728	Sequence 4 from patent US 5...	160	6e-39
gi 3990895 gb AAC84322.1 AR000745	Sequence 21 from patent US 573	159	1e-38
gi 15110183 gb AAE67847.1	Sequence 44 from patent US 6217872...	159	1e-38

gi 2486041 gb AAB74177.1 I47795	Sequence 1 from patent US 563959	156	1e-37
gi 3990884 gb AAC84311.1 AR000734	Sequence 10 from patent US 573	155	1e-37
gi 3992546 gb AAC85973.1 AR005490	Sequence 68 from patent US 574	155	2e-37
gi 14101381 gb AAE53698.1	Sequence 34 from patent US 6150087...	154	3e-37
gi 3990883 gb AAC84310.1 AR000733	Sequence 9 from patent US 5736	154	4e-37
gi 3990886 gb AAC84313.1 AR000736	Sequence 12 from patent US 573	153	7e-37
gi 33759573 gb AAQ52063.1	Sequence 37 from patent US 6593083...	149	1e-35
gi 2486055 gb AAB74191.1 I47809	Sequence 15 from patent US 56395	147	4e-35
gi 3990887 gb AAC84314.1 AR000737	Sequence 13 from patent US 573	147	4e-35
gi 14101375 gb AAE53692.1	Sequence 22 from patent US 6150087	147	4e-35
gi 3990882 gb AAC84309.1 AR000732	Sequence 8 from patent US 5736	147	7e-35
gi 3990881 gb AAC84308.1 AR000731	Sequence 7 from patent US 5736	146	8e-35
gi 3990885 gb AAC84312.1 AR000735	Sequence 11 from patent US 573	145	2e-34
gi 3990889 gb AAC84316.1 AR000739	Sequence 15 from patent US 573	145	2e-34
gi 3992550 gb AAC85977.1 AR005494	Sequence 72 from patent US 574	145	2e-34
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gi 28072519 gb AAO30427.1	Sequence 39 from patent US 6322965	144	3e-34
gi 2486051 gb AAB74187.1 I47805	Sequence 11 from patent US 56395	144	3e-34
gi 3990888 gb AAC84315.1 AR000738	Sequence 14 from patent US 573	144	3e-34
gi 3992534 gb AAC85961.1 AR005478	Sequence 56 from patent US 574	144	4e-34
gi 3990880 gb AAC84307.1 AR000730	Sequence 6 from patent US 5736	142	1e-33
gi 2486045 gb AAB74181.1 I47799	Sequence 5 from patent US 563959	142	2e-33
gi 3990891 gb AAC84318.1 AR000741	Sequence 17 from patent US 573	141	2e-33
gi 3990890 gb AAC84317.1 AR000740	Sequence 16 from patent US 573	140	4e-33
gi 3990893 gb AAC84320.1 AR000743	Sequence 19 from patent US 573	140	8e-33
gi 3990892 gb AAC84319.1 AR000742	Sequence 18 from patent US 573	139	1e-32
gi 3990894 gb AAC84321.1 AR000744	Sequence 20 from patent US 573	138	2e-32
gi 3990879 gb AAC84306.1 AR000729	Sequence 5 from patent US 5...	138	2e-32
gi 3992545 gb AAC85972.1 AR005489	Sequence 67 from patent US 574	137	7e-32
gi 2486058 gb AAB74194.1 I47812	Sequence 18 from patent US 56395	137	7e-32
gi 2486042 gb AAB74178.1 I47796	Sequence 2 from patent US 563959	136	9e-32
gi 14101434 gb AAE53751.1	Sequence 144 from patent US 6150087	134	4e-31
gi 2486043 gb AAB74179.1 I47797	Sequence 3 from patent US 563959	134	6e-31
gi 2486054 gb AAB74190.1 I47808	Sequence 14 from patent US 56395	133	9e-31
gi 2486050 gb AAB74186.1 I47804	Sequence 10 from patent US 56395	130	8e-30
gi 3992528 gb AAC85955.1 AR005472	Sequence 50 from patent US 574	128	2e-29
gi 3211585 gb AAC21345.1 I83288	Sequence 74 from patent US 57...	122	2e-27
gi 21508654 gb AAM58142.1	Sequence 4 from patent US 6379886	122	2e-27
gi 3992538 gb AAC85965.1 AR005482	Sequence 60 from patent US 574	122	2e-27
gi 3992544 gb AAC85971.1 AR005488	Sequence 66 from patent US 574	121	3e-27
gi 56568958 gb AAV99204.1	Sequence 40 from patent US 6762024...	120	5e-27
gi 56568955 gb AAV99201.1	Sequence 34 from patent US 6762024...	120	5e-27
gi 56568956 gb AAV99202.1	Sequence 36 from patent US 6762024...	120	6e-27
gi 2486044 gb AAB74180.1 I47798	Sequence 4 from patent US 563959	119	1e-26
gi 2486057 gb AAB74193.1 I47811	Sequence 17 from patent US 56395	118	3e-26
gi 3992555 gb AAC85982.1 AR005499	Sequence 77 from patent US 574	114	3e-25
gi 3211587 gb AAC21347.1 I83290	Sequence 78 from patent US 57...	111	4e-24
gi 14101387 gb AAE53704.1	Sequence 46 from patent US 6150087	111	4e-24
gi 2486053 gb AAB74189.1 I47807	Sequence 13 from patent US 56395	110	5e-24
gi 33767202 gb AAQ52964.1	Sequence 8 from patent US 6596476	110	6e-24
gi 2486049 gb AAB74185.1 I47803	Sequence 9 from patent US 563959	107	5e-23
gi 3992549 gb AAC85976.1 AR005493	Sequence 71 from patent US 574	107	6e-23
gi 5997159 gb AAE20706.1	Sequence 146 from patent US 5849532...	105	1e-22
gi 3992527 gb AAC85954.1 AR005471	Sequence 49 from patent US 574	105	2e-22
gi 3995368 gb AAC88796.1 AR012918	Sequence 14 from patent US 576	105	2e-22
gi 3992532 gb AAC85959.1 AR005476	Sequence 54 from patent US 574	105	2e-22
gi 3990924 gb AAC84351.1 AR000774	Sequence 50 from patent US 573	102	2e-21
gi 3995370 gb AAC88798.1 AR012920	Sequence 17 from patent US 576	101	4e-21
gi 3992543 gb AAC85970.1 AR005487	Sequence 65 from patent US 574	100	7e-21
gi 33767200 gb AAQ52962.1	Sequence 6 from patent US 6596476	97.4	6e-20
gi 2486056 gb AAB74192.1 I47810	Sequence 16 from patent US 56395	97.1	7e-20

gi 91126681 gb ABE13372.1	Sequence 33 from patent US 6977144	95.5	3e-19
gi 56568969 gb AAV99215.1	Sequence 62 from patent US 6762024	94.0	6e-19
gi 3992531 gb AAC85958.1 AR005475	Sequence 53 from patent US 574	93.6	8e-19
gi 10279243 emb CAC09848.1	unnamed protein product [unidenti...	92.8	1e-18
gi 3992548 gb AAC85975.1 AR005492	Sequence 70 from patent US 574	88.6	2e-17
gi 3992496 gb AAC85923.1 AR005440	Sequence 18 from patent US ...	87.4	6e-17
gi 91175838 gb ABE26532.1	Sequence 13 from patent US 7022830...	87.4	6e-17
gi 56568968 gb AAV99214.1	Sequence 60 from patent US 6762024	87.4	6e-17
gi 3992554 gb AAC85981.1 AR005498	Sequence 76 from patent US 574	87.0	8e-17
gi 10279241 emb CAC09847.1	unnamed protein product [unidenti...	86.7	1e-16
gi 42685376 gb AAS29957.1	Sequence 7 from patent US 6680059 ...	85.5	2e-16
gi 3990923 gb AAC84350.1 AR000773	Sequence 49 from patent US 573	83.6	8e-16
gi 31689218 gb AAP61070.1	Sequence 95 from patent US 6538126	82.0	2e-15
gi 3992542 gb AAC85969.1 AR005486	Sequence 64 from patent US 574	81.3	4e-15
gi 3992533 gb AAC85960.1 AR005477	Sequence 55 from patent US 574	80.9	6e-15
gi 3992526 gb AAC85953.1 AR005470	Sequence 48 from patent US 574	80.1	9e-15
gi 91126675 gb ABE13366.1	Sequence 27 from patent US 6977144	79.7	1e-14
gi 33759591 gb AAQ52081.1	Sequence 58 from patent US 6593083...	79.0	2e-14
gi 91149569 gb ABE23184.1	Sequence 2 from patent US 7009044	78.6	3e-14
gi 2491581 gb AAB79717.1 I64956	Sequence 2 from patent US 566...	78.6	3e-14
gi 40194425 gb AAR78466.1	Sequence 24 from patent US 6653127...	78.2	4e-14
gi 91126701 gb ABE13392.1	Sequence 91 from patent US 6977144	77.0	9e-14
gi 3992553 gb AAC85980.1 AR005497	Sequence 75 from patent US 574	75.9	2e-13
gi 91126657 gb ABE13348.1	Sequence 9 from patent US 6977144	75.5	2e-13
gi 514199 emb CAA01307.1	polypeptide which can be used as a ...	75.5	3e-13
gi 15149804 emb CAC50872.1	unnamed protein product [Classica...	75.5	3e-13
gi 594196 gb AAA55803.1	Sequence 39 from Patent EP 0318216 >...	75.1	3e-13
gi 33767203 gb AAQ52965.1	Sequence 9 from patent US 6596476	73.9	7e-13
gi 5997156 gb AAE20703.1	Sequence 106 from patent US 5849532...	73.9	7e-13
gi 2304757 emb CAA03388.1	unnamed protein product [Classical...	73.9	7e-13
gi 3992481 gb AAC85908.1 AR005425	Sequence 3 from patent US 5...	73.2	1e-12
gi 91126650 gb ABE13341.1	Sequence 2 from patent US 6977144	72.8	1e-12
gi 91126656 gb ABE13347.1	Sequence 8 from patent US 6977144	72.8	1e-12
gi 5957227 gb AAE07901.1	Sequence 2 from patent US 5800982	72.8	1e-12
gi 3992547 gb AAC85974.1 AR005491	Sequence 69 from patent US 574	72.0	3e-12
gi 14101368 gb AAE53685.1	Sequence 8 from patent US 6150087	72.0	3e-12
gi 3992530 gb AAC85957.1 AR005474	Sequence 52 from patent US 574	70.9	5e-12
gi 5957226 gb AAE07900.1	Sequence 1 from patent US 5800982	70.9	5e-12
gi 5992019 gb AAE18828.1	Sequence 30 from patent US 5843752 ...	70.9	5e-12
gi 3992537 gb AAC85964.1 AR005481	Sequence 59 from patent US 574	67.8	5e-11
gi 3992541 gb AAC85968.1 AR005485	Sequence 63 from patent US 574	66.2	1e-10
gi 3992495 gb AAC85922.1 AR005439	Sequence 17 from patent US 574	65.9	2e-10
gi 91126658 gb ABE13349.1	Sequence 10 from patent US 6977144	65.5	2e-10
gi 5992020 gb AAE18829.1	Sequence 31 from patent US 5843752 ...	65.5	3e-10
gi 5944572 gb AAE02648.1	Sequence 3 from patent US 5861297	65.1	3e-10
gi 3991313 gb AAC84740.1 AR001744	Sequence 3 from patent US 5739	65.1	3e-10
gi 33767205 gb AAQ52967.1	Sequence 11 from patent US 6596476	65.1	4e-10
gi 15110182 gb AAE67846.1	Sequence 42 from patent US 6217872...	62.8	2e-09
gi 3990922 gb AAC84349.1 AR000772	Sequence 48 from patent US 573	60.8	5e-09
gi 14114664 gb AAE58451.1	Sequence 2 from patent US 6180109	60.8	6e-09
gi 91126659 gb ABE13350.1	Sequence 11 from patent US 6977144	57.4	6e-08
gi 3992529 gb AAC85956.1 AR005473	Sequence 51 from patent US 574	57.0	9e-08
gi 3992499 gb AAC85926.1 AR005443	Sequence 21 from patent US ...	55.8	2e-07
gi 1829783 gb AAB44237.1	Sequence 11 from patent US 5582968	55.8	2e-07
gi 5997160 gb AAE20707.1	Sequence 148 from patent US 5849532...	55.8	2e-07
gi 33767204 gb AAQ52966.1	Sequence 10 from patent US 6596476	55.5	3e-07
gi 40160954 gb AAR67306.1	Sequence 25 from patent US 6635257	55.1	3e-07
gi 23316922 gb AAN21417.1	Sequence 17 from patent US 6416946...	55.1	4e-07
gi 28072522 gb AAO30430.1	Sequence 42 from patent US 6322965	55.1	4e-07
gi 33767206 gb AAQ52968.1	Sequence 12 from patent US 6596476...	54.3	5e-07
gi 53985916 gb AAV26905.1	Sequence 17 from patent US 6780967...	54.3	6e-07

gi 40115542 gb AAR55544.1	Sequence 63 from patent US 6613530	54.3	6e-07
gi 91126661 gb ABE13352.1	Sequence 13 from patent US 6977144	53.5	9e-07
gi 5957229 gb AAE07903.1	Sequence 4 from patent US 5800982	52.8	2e-06
gi 3990925 gb AAC84352.1 AR000775	Sequence 51 from patent US 573	52.4	2e-06
gi 5957228 gb AAE07902.1	Sequence 3 from patent US 5800982	52.4	2e-06
gi 15554476 emb CAC69563.1	unnamed protein product [synthetic c	51.2	5e-06
gi 15554472 emb CAC69561.1	unnamed protein product [synthetic c	51.2	5e-06
gi 15554470 emb CAC69560.1	unnamed protein product [synthetic c	51.2	5e-06
gi 15554488 emb CAC69569.1	unnamed protein product [synthetic c	50.8	6e-06
gi 15554468 emb CAC69559.1	unnamed protein product [synthetic c	50.8	6e-06
gi 15554466 emb CAC69558.1	unnamed protein product [synthetic c	50.8	6e-06
gi 3990913 gb AAC84340.1 AR000763	Sequence 39 from patent US 573	50.4	7e-06
gi 3990914 gb AAC84341.1 AR000764	Sequence 40 from patent US 573	50.4	7e-06
gi 33759590 gb AAQ52080.1	Sequence 55 from patent US 6593083...	50.4	9e-06
gi 3990903 gb AAC84330.1 AR000753	Sequence 29 from patent US 573	49.3	2e-05
gi 3990902 gb AAC84329.1 AR000752	Sequence 28 from patent US 573	49.3	2e-05
gi 3990904 gb AAC84331.1 AR000754	Sequence 30 from patent US 573	48.9	2e-05
gi 15554474 emb CAC69562.1	unnamed protein product [synthetic c	48.9	3e-05
gi 15554478 emb CAC69564.1	unnamed protein product [synthetic c	48.1	4e-05
gi 83329648 gb ABC06928.1	Sequence 52 from patent US 6960659	48.1	4e-05
gi 3990915 gb AAC84342.1 AR000765	Sequence 41 from patent US 573	47.8	5e-05
gi 56569106 gb AAV99352.1	Sequence 272 from patent US 676202...	47.4	7e-05
gi 47255634 gb AAT22908.1	Sequence 148 from patent US 670982...	47.4	7e-05
gi 492886 emb CAA00808.1	unnamed protein product [Potato virus	46.2	1e-04
gi 14101400 gb AAE53717.1	Sequence 70 from patent US 6150087...	46.2	2e-04
gi 14101367 gb AAE53684.1	Sequence 2 from patent US 6150087 ...	46.2	2e-04
gi 47267560 gb AAT26432.1	Sequence 65 from patent US 6720166...	45.8	2e-04
gi 15554486 emb CAC69568.1	unnamed protein product [synthetic c	45.4	2e-04
gi 15554484 emb CAC69567.1	unnamed protein product [synthetic c	45.4	2e-04
gi 47255607 gb AAT22881.1	Sequence 121 from patent US 670982...	45.1	3e-04
gi 42668573 gb AAS24361.1	Sequence 121 from patent US 666738...	45.1	3e-04
gi 33767207 gb AAQ52969.1	Sequence 13 from patent US 6596476	45.1	3e-04
gi 14101954 gb AAE54271.1	Sequence 771 from patent US 6150087	45.1	3e-04
gi 15554482 emb CAC69566.1	unnamed protein product [synthetic c	45.1	4e-04
gi 15554480 emb CAC69565.1	unnamed protein product [synthetic c	45.1	4e-04
gi 47234811 gb AAT13745.1	Sequence 53 from patent US 6696281...	44.7	5e-04
gi 1829777 gb AAB44231.1	Sequence 5 from patent US 5582968	44.3	6e-04
gi 23316923 gb AAN21418.1	Sequence 18 from patent US 6416946...	44.3	7e-04
gi 3995362 gb AAC88790.1 AR012912	Sequence 7 from patent US 5763	44.3	7e-04
gi 56568990 gb AAV99236.1	Sequence 103 from patent US 6762024	43.9	7e-04
gi 23315947 gb AAN20959.1	Sequence 204 from patent US 6413517	43.9	8e-04
gi 56569109 gb AAV99355.1	Sequence 275 from patent US 6762024	43.5	0.001
gi 3995363 gb AAC88791.1 AR012913	Sequence 8 from patent US 5763	43.5	0.001
gi 7224497 gb AAE24664.1	Sequence 44 from patent US 5910405	43.5	0.001
gi 47267488 gb AAT26396.1	Sequence 16 from patent US 6720166...	43.1	0.001
gi 15554464 emb CAC69557.1	unnamed protein product [synthetic c	42.7	0.002
gi 15554462 emb CAC69556.1	unnamed protein product [synthetic c	42.7	0.002
gi 56568989 gb AAV99235.1	Sequence 102 from patent US 6762024	42.4	0.002
gi 2296952 emb CAA02588.1	unnamed protein product [Hepatitis...	42.4	0.002
gi 23315943 gb AAN20955.1	Sequence 200 from patent US 6413517	42.4	0.003
gi 2296950 emb CAA02587.1	unnamed protein product [Hepatitis...	41.6	0.004
gi 6065683 emb CAB58544.1	unnamed protein product [Dengue virus	41.6	0.004
gi 42685374 gb AAS29955.1	Sequence 5 from patent US 6680059 ...	41.2	0.005
gi 40160956 gb AAR67308.1	Sequence 27 from patent US 6635257	41.2	0.005
gi 3990918 gb AAC84345.1 AR000768	Sequence 44 from patent US 573	40.0	0.010
gi 33758793 gb AAQ51732.1	Sequence 1 from patent US 6592871 ...	39.7	0.013
gi 3990917 gb AAC84344.1 AR000767	Sequence 43 from patent US 573	39.7	0.013
gi 3990916 gb AAC84343.1 AR000766	Sequence 42 from patent US 573	39.7	0.013
gi 33767201 gb AAQ52963.1	Sequence 7 from patent US 6596476	39.3	0.019
gi 2296962 emb CAA02593.1	unnamed protein product [Hepatitis...	39.3	0.020
gi 40082535 gb AAR41089.1	Sequence 4359 from patent US 6605709	39.3	0.021

gi 45503032 emb CAF86306.1	unnamed protein product [Homo sapien	38.9	0.021
gi 23315942 gb AAN20954.1	Sequence 199 from patent US 6413517	38.9	0.024
gi 2296958 emb CAA02591.1	unnamed protein product [Hepatitis...	38.9	0.026
gi 40160955 gb AAR67307.1	Sequence 26 from patent US 6635257	38.5	0.031
gi 3995364 gb AAC88792.1 AR012914	Sequence 9 from patent US 5763	38.1	0.037
gi 27647036 emb CAD60138.1	unnamed protein product [Flavivir...	38.1	0.039
gi 2296960 emb CAA02592.1	unnamed protein product [Hepatitis...	38.1	0.039
gi 40103007 gb AAR48358.1	Sequence 8075 from patent US 6610836	38.1	0.040
gi 56568984 gb AAV99230.1	Sequence 97 from patent US 6762024...	38.1	0.041
gi 47255593 gb AAT22867.1	Sequence 107 from patent US 670982...	38.1	0.041
gi 20224835 gb AAE88376.1	Sequence 44 from patent US 6335435...	38.1	0.044
gi 20224829 gb AAE88370.1	Sequence 38 from patent US 6335435...	38.1	0.044
gi 67582840 gb AAY71465.1	Sequence 1512 from patent US 68874...	37.7	0.050
gi 56627913 gb AAW06247.1	Sequence 7 from patent US 6797809 ...	37.7	0.061
gi 56568985 gb AAV99231.1	Sequence 98 from patent US 6762024	37.4	0.070
gi 1829782 gb AAB44236.1	Sequence 10 from patent US 5582968	37.0	0.086
gi 40160953 gb AAR67305.1	Sequence 24 from patent US 6635257	37.0	0.095
gi 33741959 gb AAQ42691.1	Sequence 75 from patent US 6583112	37.0	0.10
gi 5972345 gb AAE12236.1	Sequence 77 from patent US 5824501 ...	37.0	0.10
gi 23316924 gb AAN21419.1	Sequence 19 from patent US 6416946...	36.6	0.11
gi 23315996 gb AAN21008.1	Sequence 253 from patent US 6413517	36.6	0.13
gi 2296956 emb CAA02590.1	unnamed protein product [Hepatitis...	36.2	0.15
gi 47255579 gb AAT22853.1	Sequence 93 from patent US 6709828...	35.8	0.19
gi 40192138 gb AAR77444.1	Sequence 93 from patent US 6649735	35.8	0.19
gi 23316925 gb AAN21420.1	Sequence 20 from patent US 6416946...	35.8	0.23
gi 91175839 gb ABE26533.1	Sequence 14 from patent US 7022830...	35.8	0.23
gi 53957550 gb AAV07547.1	Sequence 19504 from patent US 6747137	35.0	0.33
gi 20224830 gb AAE88371.1	Sequence 39 from patent US 6335435...	35.0	0.36
gi 5972344 gb AAE12235.1	Sequence 76 from patent US 5824501 ...	35.0	0.36
gi 59738755 gb AAW92929.1	Sequence 10492 from patent US 6833447	34.3	0.56
gi 91175841 gb ABE26535.1	Sequence 16 from patent US 7022830...	34.3	0.67
gi 91175846 gb ABE26540.1	Sequence 21 from patent US 7022830...	33.5	0.92
gi 42681965 gb AAS28430.1	Sequence 3572 from patent US 6673910	33.1	1.2
gi 91175843 gb ABE26537.1	Sequence 18 from patent US 7022830...	33.1	1.3
gi 23315918 gb AAN20930.1	Sequence 175 from patent US 6413517	33.1	1.3

Alignments

Get selected sequences	Select all	Deselect all	Distance tree of results
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> gi|594200|gb|AAA55807.1| Sequence 53 from Patent EP 0318216
 gi|592429|gb|AAA54036.1| Sequence 9 from Patent WO 8904669

Length=2261

Score = 1303 bits (3372), Expect = 0.0, Method: Composition-based stats.
 Identities = 683/685 (99%), Positives = 683/685 (99%), Gaps = 0/685 (0%)

Query 1	APITAYAQQTGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct 402	APITAYAQQTGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	461
Query 61	TRTIASPKGPVIQMYTNVDQDLVGPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct 462	TRTIASPKGPVIQMYTNVDQDLVGPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRG	521
Query 121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct 522	DSRGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	581



results of BLAST

BLASTP 2.2.14 [May-07-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference:

Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

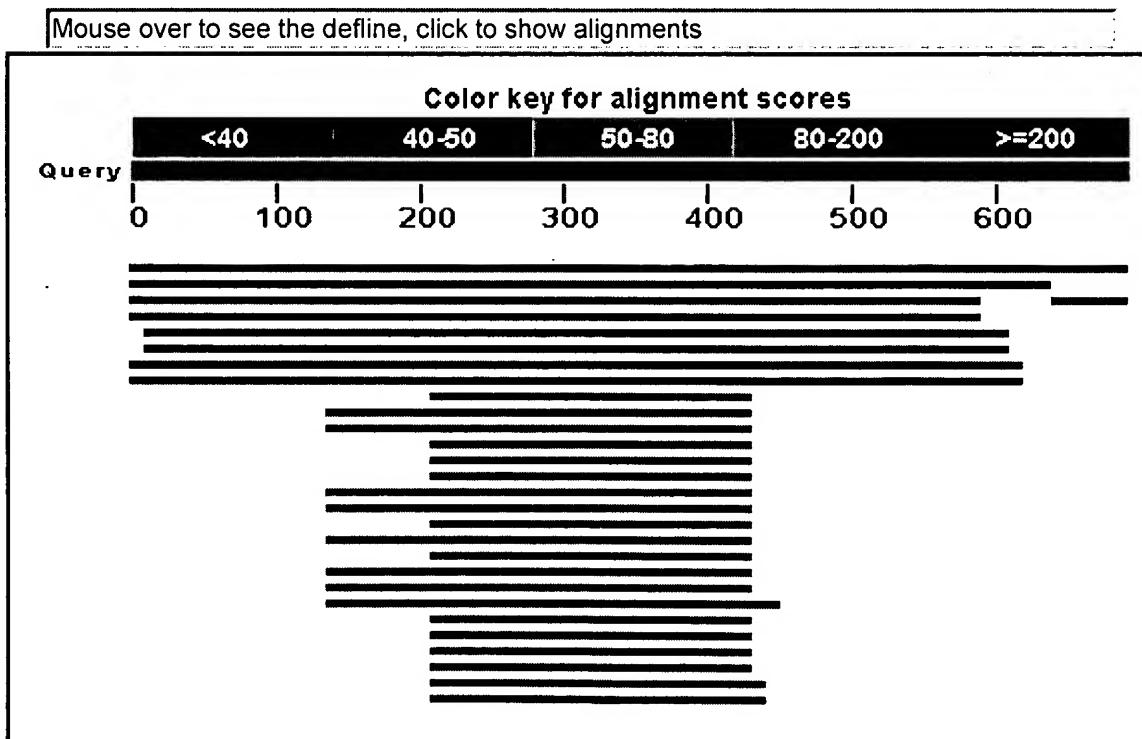
RID: 1153602022-27610-106952644218.BLASTQ1

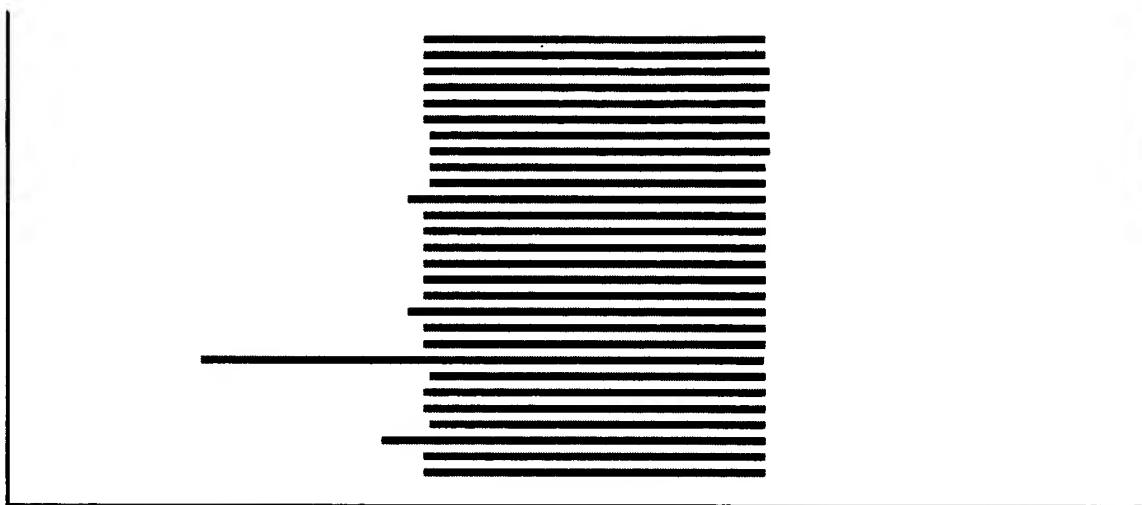
Database: NCBI Protein Reference Sequences
2,389,055 sequences; 864,113,167 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=685

Distribution of 100 Blast Hits on the Query Sequence





Distance tree of results NEW

Sequences producing significant alignments:		Score (Bits)	E Value	
gi 22129793 ref NP_671491.1 	polyprotein [Hepatitis C virus]	1286	0.0	G
gi 28921568 ref NP_803144.1 	NS3 protease/helicase' [Hepatitis C	1167	0.0	G
gi 9628102 ref NP_056931.1 	polyprotein [Hepatitis GB virus B]	400	1e-109	G
gi 26251699 ref NP_757357.1 	putative NS3 proteinase/ATPase/heli	393	8e-108	G
gi 9628706 ref NP_043570.1 	polyprotein precursor [GB virus C/He	387	8e-106	G
gi 28971393 ref NP_803205.1 	NS3 proteinase/ATPase/helicase [GB	382	3e-104	G
gi 9629719 ref NP_045010.1 	polyprotein precursor [Hepatitis GB	359	2e-97	G
gi 28971401 ref NP_803213.1 	NS3 proteinase/ATPase/helicase [Hep	352	2e-95	G
gi 26053627 ref NP_751925.1 	NS4A protein [Hepatitis C virus]	85.5	5e-15	G
gi 9626650 ref NP_040937.1 	polyprotein [Bovine viral diarrhea v	79.7	3e-13	G
gi 20198946 ref NP_620062.1 	polyprotein [Border disease virus 1	79.3	4e-13	G
gi 27883894 ref NP_777540.1 	nonstructural protein NS2-3 [Border	79.0	5e-13	G
gi 27777749 ref NP_776266.1 	nonstructural protein NS2-3 [Bovine	78.6	6e-13	G
gi 27777750 ref NP_776267.1 	nonstructural protein NS3 [Bovine v	77.8	1e-12	G
gi 20178631 ref NP_620051.1 	polyprotein [Pestivirus Reindeer-1]	76.6	3e-12	G
gi 27883895 ref NP_777541.1 	nonstructural protein NS3 [Border d	76.6	3e-12	G
gi 20178633 ref NP_620053.1 	polyprotein [Pestivirus Giraffe-1]	76.3	3e-12	G
gi 27885135 ref NP_777514.1 	nonstructural protein NS2-3; NTP...	75.9	4e-12	G
gi 27885118 ref NP_777527.1 	nonstructural protein NS2-3; NTP...	75.1	8e-12	G
gi 27885136 ref NP_777515.1 	nonstructural protein NS3; NTPas...	74.3	1e-11	G
gi 12657942 ref NP_075354.1 	polyprotein [Classical swine fever	74.3	1e-11	G
gi 27885150 ref NP_777501.1 	nonstructural protein NS2-3 [Classi	73.6	2e-11	G
gi 27885119 ref NP_777528.1 	nonstructural protein NS3; NTPas...	73.2	3e-11	G
gi 27885151 ref NP_777502.1 	nonstructural protein NS3 [Classica	71.2	1e-10	G
gi 9629507 ref NP_044731.1 	putative polyprotein [Bovine viral d	71.2	1e-10	G
gi 27885409 ref NP_777488.1 	nonstructural protein NS2-3; NTP...	70.9	1e-10	G
gi 27885410 ref NP_777489.1 	nonstructural protein NS3; NTPas...	69.3	4e-10	G
gi 9790345 ref NP_062908.1 	polyprotein [Tobacco etch virus]	65.1	8e-09	G
gi 25013637 ref NP_734211.1 	CI protein [Tobacco etch virus]	65.1	8e-09	G

gi 9633629 ref NP_051161.1	polyprotein [Japanese yam mosaic virus]	62.8	4e-08	G
gi 25013886 ref NP_734227.1	CI protein [Japanese yam mosaic virus]	62.0	6e-08	G
gi 9629731 ref NP_045216.1	polyprotein [Sweet potato feathery mottling virus]	61.2	1e-07	G
gi 25013777 ref NP_734313.1	CI protein [Sweet potato feathery mottling virus]	60.5	2e-07	G
gi 21427634 ref NP_659018.1	polyprotein [Cowpea aphid-borne mosaic virus]	59.7	4e-07	G
gi 25013523 ref NP_734383.1	CI protein [Cowpea aphid-borne mosaic virus]	59.7	4e-07	G
gi 45004655 ref NP_982308.1	polyprotein [Chilli veinal mottle virus]	58.5	7e-07	G
gi 45004660 ref NP_982339.1	cytoplasmic inclusion protein [Chilli veinal mottle virus]	58.5	7e-07	G
gi 18677788 ref NP_570723.1	polyprotein [Bean common mosaic virus]	57.0	2e-06	G
gi 25013493 ref NP_734117.1	CI protein [Bean common mosaic virus]	56.6	3e-06	G
gi 9626509 ref NP_040807.1	polyprotein [Plum pox virus]	56.2	4e-06	G
gi 51949946 ref YP_077181.1	polyprotein [Watermelon mosaic virus]	56.2	4e-06	G
gi 51949950 ref YP_077271.1	cylindrical inclusion protein [Watermelon mosaic virus]	56.2	4e-06	G
gi 56407094 ref NP_062866.2	polyprotein [Turnip mosaic virus]	55.8	4e-06	G
gi 25013653 ref NP_734217.1	CI protein [Turnip mosaic virus]	55.8	4e-06	G
gi 20087055 ref NP_613274.1	polyprotein [Dasheen mosaic virus]	55.8	5e-06	G
gi 25013787 ref NP_734107.1	CI protein [Dasheen mosaic virus]	55.8	5e-06	G
gi 25013583 ref NP_734343.1	CI protein [Plum pox virus]	55.5	6e-06	G
gi 9627035 ref NP_041276.1	polyprotein [Pepper mottle virus]	55.1	9e-06	G
gi 25013572 ref NP_734432.1	CI protein [Pepper mottle virus]	55.1	9e-06	G
gi 9633623 ref NP_051124.1	polyprotein [Murray Valley encephalitis virus]	53.9	2e-05	G
gi 85677474 ref YP_459919.1	polyprotein [East Asian Passiflora virus]	53.9	2e-05	G
gi 25013612 ref NP_734196.1	CI protein [Soybean mosaic virus]	53.5	2e-05	G
gi 12018226 ref NP_072165.1	polyprotein precursor [Soybean mosaic virus]	53.5	2e-05	G
gi 21431572 ref NP_659008.1	polyprotein [Potato virus V]	53.1	3e-05	G
gi 71647083 ref YP_271857.1	polyprotein [Wisteria vein mosaic virus]	53.1	3e-05	G
gi 39163615 ref NP_945133.1	polyprotein [Lily mottle virus]	53.1	3e-05	G
gi 39163620 ref NP_945140.1	CI protein [Lily mottle virus]	53.1	3e-05	G
gi 22550316 ref NP_689391.1	polyprotein [Montana myotis leukoen]	53.1	3e-05	G
gi 24418986 ref NP_722535.1	NS3; nonstructural protein 3; pr...	53.1	3e-05	G
gi 25013853 ref NP_734373.1	CI protein [Potato virus V]	53.1	3e-05	G
gi 90093257 ref YP_529494.1	CI protein [Konjak mosaic virus]	52.8	4e-05	G
gi 90093252 ref YP_529485.1	polyprotein [Konjak mosaic virus]	52.8	4e-05	G
gi 27669994 ref NP_775649.1	non-structural protein NS3 [Montgomery virus]	52.0	6e-05	G
gi 20153340 ref NP_619667.1	polyprotein [Lettuce mosaic virus]	52.0	8e-05	G
gi 19881395 ref NP_612218.1	polyprotein [Bean yellow mosaic virus]	51.6	8e-05	G
gi 25013503 ref NP_734177.1	CI protein [Bean yellow mosaic virus]	51.6	8e-05	G
gi 40254028 ref NP_954611.1	polyprotein [Beet mosaic virus]	51.6	9e-05	G
gi 40254033 ref NP_954623.1	CI protein [Beet mosaic virus]	51.6	9e-05	G
gi 25013533 ref NP_734157.1	CI protein [Lettuce mosaic virus]	51.6	9e-05	G
gi 25013916 ref NP_734353.1	CI protein [Bean common mosaic necrotic virus]	51.6	9e-05	G
gi 21553929 ref NP_660175.1	polyprotein [Bean common mosaic necrotic virus]	51.6	9e-05	G
gi 20153408 ref NP_619668.1	polyprotein [Johnsongrass mosaic virus]	51.2	1e-04	G
gi 25013812 ref NP_734402.1	CI protein [Johnsongrass mosaic virus]	51.2	1e-04	G
gi 76803356 ref YP_331413.1	polyprotein [Shallot yellow stripe virus]	50.4	2e-04	G
gi 76803355 ref YP_331412.1	polyprotein [Shallot yellow stripe virus]	50.4	2e-04	G
gi 76803361 ref YP_331418.1	CI protein [Shallot yellow stripe virus]	50.4	2e-04	G
gi 20428637 ref NP_620483.1	polyprotein [Cocksfoot streak virus]	50.4	2e-04	G

gi 25014042 ref NP_734393.1	CI protein [Cocksfoot streak virus]	50.1	2e-04	G
gi 17059638 ref NP_477522.1	polyprotein [Zucchini yellow mosaic	50.1	2e-04	G
gi 25013663 ref NP_734187.1	CI protein [Zucchini yellow mosaic	50.1	2e-04	G
gi 48843533 ref YP_025107.1	polyprotein [Hordeum mosaic virus]	50.1	3e-04	G
gi 20087031 ref NP_613273.1	polyprotein [Clover yellow vein vir	49.3	4e-04	G
gi 25013513 ref NP_734167.1	CI protein [Clover yellow vein viru	49.3	4e-04	G
gi 9626461 ref NP_059434.1	hypothetical protein JEVgp1 [Japanes	49.3	5e-04	G
gi 51101432 ref YP_063390.1	CI protein [Hordeum mosaic virus]	48.9	6e-04	G
gi 27696332 ref NP_775670.1	non-structural protein NS3 [Japanes	48.5	7e-04	G
gi 56692442 ref YP_164264.1	polyprotein precursor [Usutu virus]	48.5	8e-04	
gi 21492612 ref NP_659729.1	polyprotein [Potato virus A]	48.1	0.001	G
gi 25013593 ref NP_734363.1	CI protein [Potato virus A]	48.1	0.001	G
gi 9627243 ref NP_041725.1	cell fusing agent polyprotein [Cell	48.1	0.001	G
gi 9626682 ref NP_056776.1	hypothetical protein DENNgp1 [Dengue	47.8	0.001	G
gi 27366084 ref NP_761612.1	HrpA-like helicase [Vibrio vulnific	47.8	0.001	G
gi 25059134 ref NP_739587.1	NS3 protein [Dengue virus type 2]	47.8	0.001	G
gi 37679649 ref NP_934258.1	HrpA-like helicase [Vibrio vulnific	47.4	0.002	G
gi 56692450 ref YP_164814.1	NS3 [Usutu virus]	47.4	0.002	
gi 9629497 ref NP_044727.1	polyprotein [Ryegrass mosaic virus]	47.4	0.002	G
gi 9628430 ref NP_056765.1	polyprotein [Pea seed-borne mosaic v	47.4	0.002	G
gi 25013563 ref NP_734423.1	CI protein [Pea seed-borne mosaic v	47.0	0.002	G
gi 18652417 ref NP_570725.1	polyprotein [Scallion mosaic virus]	47.0	0.002	G
gi 25014000 ref NP_734127.1	CI protein [Scallion mosaic virus]	47.0	0.002	G
gi 25013863 ref NP_734323.1	CI protein [Ryegrass mosaic virus]	47.0	0.002	G
gi 20177456 ref NP_619758.1	polyprotein [Modoc virus]	46.6	0.003	G
gi 48237788 ref YP_022751.1	polyprotein [Yam mosaic virus]	46.2	0.003	G
gi 33620714 ref NP_891560.1	polyprotein precursor [Kamiti River	46.2	0.003	G
gi 27735345 ref NP_776044.1	putative non-structural protein NS3	46.2	0.003	G
gi 25013602 ref NP_734246.1	CI protein [Potato virus Y]	46.2	0.003	G
gi 9627729 ref NP_056759.1	polyprotein [Potato virus Y]	46.2	0.003	G
gi 20178609 ref NP_620044.1	polyprotein [Rio Bravo virus]	46.2	0.004	G
gi 25013641 ref NP_734331.1	CI protein [Tobacco vein mottling v	46.2	0.004	G
gi 9629180 ref NP_056867.1	polyprotein [Tobacco vein mottling v	46.2	0.004	G
gi 28492879 ref NP_787937.1	polyprotein [Peru tomato mosaic vir	46.2	0.004	G
gi 28519945 ref NP_787942.1	CI protein [Peru tomato mosaic viru	46.2	0.004	G
gi 48249201 ref YP_022756.1	CI protein [Yam mosaic virus]	45.8	0.004	G
gi 20070096 ref NP_612585.1	polyprotein [Brome streak mosaic vi	45.8	0.004	G
gi 25013906 ref NP_734257.1	CI protein [Brome streak mosaic vir	45.8	0.004	G
gi 27735367 ref NP_776076.1	non-structural protein NS3 [Rio Bra	45.4	0.006	G
gi 12084823 ref NP_073286.1	polyprotein precursor [Dengue virus	45.4	0.006	
gi 9626684 ref NP_040961.1	hypothetical protein [Dengue virus t	45.4	0.006	
gi 73671175 ref NP_740321.1	NS3 protein [Dengue virus type 4]	45.1	0.007	
gi 37695586 ref NP_937777.1	NS3 protein [Kamiti River virus]	45.1	0.008	G
gi 25121728 ref NP_740264.1	non-structural protein 3 [Modoc vir	45.1	0.008	G
gi 9627245 ref NP_041726.1	polyprotein precursor [Yellow fever	44.7	0.011	
gi 15595172 ref NP_212961.1	ATP-dependent helicase (hrpA) [Borr	44.7	0.012	
gi 68299604 ref YP_249455.1	polyprotein [Pennisetum mosaic viru	44.3	0.013	
gi 88861126 ref ZP_01135760.1	ATP-dependent DNA helicase [Pseud	44.3	0.015	

gi 25140981 ref NP_741959.1	polyprotein [Wild potato mosaic vi	43.9	0.016	G
gi 76650592 ref XP_885404.1	PREDICTED: similar to Putative p...	43.9	0.017	G
gi 76650590 ref XP_885374.1	PREDICTED: similar to Putative p...	43.9	0.017	G
gi 76650588 ref XP_885353.1	PREDICTED: similar to Putative p...	43.9	0.017	G
gi 76650586 ref XP_885324.1	PREDICTED: similar to Putative p...	43.9	0.017	G
gi 76650584 ref XP_582847.2	PREDICTED: similar to Putative p...	43.9	0.017	G
gi 76650582 ref XP_885275.1	PREDICTED: similar to Putative p...	43.9	0.017	G
gi 76650576 ref XP_872459.1	PREDICTED: similar to Putative p...	43.9	0.017	G
gi 27735293 ref NP_776005.1	non-structural protein NS3 [Yellow	43.9	0.017	G
gi 50944385 ref XP_481720.1	RNA helicase-like [Oryza sativa (ja	43.9	0.017	U G
gi 47059171 ref NP_997661.1	DEAH (Asp-Glu-Ala-His) box polypept	43.9	0.020	U G
gi 30794426 ref NP_081263.1	DEAH (Asp-Glu-Ala-His) box polypept	43.9	0.020	U G
gi 25141242 ref NP_741973.1	CI protein [Wild potato mosaic viru	43.5	0.024	G
gi 27383239 ref NP_774768.1	helicase [Bradyrhizobium japonicum	43.1	0.028	G
gi 20178607 ref NP_620045.1	polyprotein [Apoi virus]	43.1	0.029	G
gi 4503293 ref NP_003578.1	DEAH (Asp-Glu-Ala-His) box polypepti	43.1	0.030	U G
gi 108860675 ref NP_001035839.1	DEAH (Asp-Glu-Ala-His) box poly	43.1	0.030	G
gi 73972117 ref XP_856831.1	PREDICTED: similar to Putative p...	43.1	0.033	G
gi 73972115 ref XP_856794.1	PREDICTED: similar to Putative p...	43.1	0.033	G
gi 73972113 ref XP_856752.1	PREDICTED: similar to Putative p...	43.1	0.033	G
gi 73972109 ref XP_538827.2	PREDICTED: similar to Putative p...	43.1	0.033	G
gi 11528014 ref NP_041724.2	polyprotein precursor [West Nile vi	43.1	0.035	G
gi 71077358 ref XP_771193.1	Giardia lamblia ATCC 50803 pre-m...	42.7	0.036	G
gi 9626686 ref NP_059433.1	polyprotein [Dengue virus type 1]	42.7	0.036	
gi 22329903 ref NP_174527.2	EMB2733; ATP binding / ATP-depen...	42.7	0.039	U G
gi 51599078 ref YP_073266.1	ATP-dependent helicase [Borrelia ga	42.7	0.040	G
gi 27735306 ref NP_776018.1	non-structural protein NS3 [West Ni	42.7	0.041	G
gi 25014066 ref NP_722463.1	nonstructural protein 3 [Dengue vir	42.7	0.041	
gi 18652415 ref NP_570724.1	polyprotein [Sugarcane mosaic virus	42.4	0.052	G
gi 18490053 ref NP_569138.1	polyprotein [Maize dwarf mosaic vir	42.4	0.059	G
gi 19112478 ref NP_595686.1	hypothetical protein SPBC19C2.01...	42.0	0.067	G
gi 76650580 ref XP_885249.1	PREDICTED: similar to Putative p...	42.0	0.073	G
gi 96980661 ref YP_610949.1	polyprotein [Daphne virus Y]	42.0	0.076	
gi 96980666 ref YP_611115.1	CI protein [Daphne virus Y]	41.6	0.085	
gi 69950831 ref ZP_00638649.1	ATP-dependent helicase HrpB [S...	41.6	0.090	
gi 86147501 ref ZP_01065812.1	putative ATP-dependent helicase [41.6	0.093	
gi 25013543 ref NP_734147.1	CI (cytoplasmic inclusion) protein	41.6	0.097	G
gi 25013623 ref NP_734137.1	CI protein [Sugarcane mosaic virus]	41.2	0.10	G
gi 84391226 ref ZP_00991557.1	putative ATP-dependent helicase [41.2	0.11	
gi 91786081 ref YP_547033.1	ATP-dependent DNA helicase RecQ [Po	41.2	0.11	G
gi 73972111 ref XP_856707.1	PREDICTED: similar to Putative p...	41.2	0.11	G
gi 110595523 ref ZP_01383854.1	ATP-dependent DNA helicase, R...	41.2	0.11	
gi 27697401 ref NP_775684.1	non-structural protein NS3 [Apoi vi	41.2	0.12	G
gi 83648495 ref YP_436930.1	ATP-dependent helicase HrpB [Hahell	40.8	0.14	G
gi 77953536 ref ZP_00817943.1	ATP-dependent helicase HrpB [Mari	40.4	0.19	
gi 24642763 ref NP_573208.1	CG8915-PA [Drosophila melanogaster]	40.4	0.20	U G
gi 83815480 ref YP_446839.1	ATP-dependent helicase HrpB [Salini	40.4	0.21	G
gi 42569631 ref NP_181077.2	ATP binding / ATP-dependent RNA ...	40.4	0.22	U G

gi 21449931 ref NP_659391.1	polyprotein [Sorghum mosaic virus]	40.4	0.22	G
gi 47574071 ref ZP_00244108.1	COG0514: Superfamily II DNA he...	40.4	0.22	
gi 25013836 ref NP_734413.1	CI protein [Peanut mottle virus]	40.4	0.22	G
gi 15808064 ref NP_068348.2	polyprotein [Peanut mottle virus]	40.4	0.22	G
gi 25013826 ref NP_734087.1	CI protein [Sorghum mosaic virus]	40.0	0.27	G
gi 37651480 ref NP_932608.1	polyprotein [Oat necrotic mottle vi	39.7	0.32	G
gi 38304205 ref NP_940826.1	CI protein [Oat necrotic mottle vir	39.7	0.32	G
gi 32490549 ref NP_870995.1	polyprotein [Papaya leaf-distortion	39.7	0.33	G
gi 32493282 ref NP_871732.1	CI [Papaya leaf-distortion mosaic p	39.7	0.33	G
gi 89362514 ref ZP_01200321.1	ATP-dependent helicase HrpB [Xant	39.7	0.33	
gi 75209551 ref ZP_00709772.1	COG0514: Superfamily II DNA helic	39.7	0.33	
gi 50931311 ref XP_475183.1	putative DEAD/DEAH RNA helicase ...	39.7	0.36	G
gi 24432114 ref NP_722551.1	polyprotein [Alkhurma virus]	39.7	0.37	G
gi 33112011 ref NP_872627.1	polyprotein [Yokose virus]	39.3	0.42	G
gi 27545511 ref NP_775474.1	non-structural protein NS3 [Alkhurm	39.3	0.43	G
gi 33589254 ref NP_878909.1	polyprotein [Omsk hemorrhagic fever	39.3	0.44	G
gi 9629245 ref NP_056758.1	polyprotein [Papaya ringspot virus]	39.3	0.46	G
gi 25013553 ref NP_734237.1	CI protein [Papaya ringspot virus]	39.3	0.46	G
gi 109471230 ref XP_001068289.1	PREDICTED: similar to DEAH (...)	39.3	0.47	G
gi 9630316 ref NP_046741.1	polyprotein [Wheat streak mosaic vir	39.3	0.49	G
gi 25013803 ref NP_734269.1	CI protein [Wheat streak mosaic vir	39.3	0.49	G
gi 6322772 ref NP_012845.1	Predominantly nucleolar DEAH-box ...	39.3	0.49	G
gi 53715360 ref YP_101352.1	ATP-dependent DNA helicase RecQ ...	39.3	0.50	G
gi 51242947 ref NP_001003715.1	RecQ protein-like 5 isoform 2 [H	38.9	0.52	U G
gi 84995412 ref XP_952428.1	ATP-dependent helicase [Theileria a	38.9	0.53	G
gi 51242943 ref NP_001003716.1	RecQ protein-like 5 isoform 3 [H	38.9	0.55	U G
gi 71838030 ref ZP_00677792.1	ATP-dependent helicase HrpB [Pelo	38.9	0.56	
gi 20522133 ref NP_620656.1	polyprotein [Sweet potato mild mott	38.9	0.58	G
gi 25013876 ref NP_734287.1	CI protein [Sweet potato mild mottl	38.9	0.59	G
gi 21919420 ref NP_665685.1	DEAH (Asp-Glu-Ala-His) box polypept	38.9	0.63	U G
gi 90419404 ref ZP_01227314.1	putative ATP-dependent DNA helica	38.9	0.64	
gi 42525842 ref NP_970940.1	ATP-dependent DNA helicase RecQ ...	38.5	0.68	G
gi 37559066 ref NP_932089.1	non-structural protein NS3 [Omsk he	38.5	0.70	G
gi 58264732 ref XP_569522.1	pre-mRNA splicing factor [Crypto...	38.5	0.71	G
gi 78692610 ref ZP_00857124.1	ATP-dependent DNA helicase Rec...	38.5	0.76	
gi 71675635 ref ZP_00673379.1	ATP-dependent DNA helicase Rec...	38.5	0.78	
gi 88810592 ref ZP_01125849.1	Lhr-like helicase [Nitrococcus mo	38.5	0.82	
gi 32490547 ref NP_871002.1	polyprotein [Onion yellow dwarf vir	38.5	0.83	G
gi 32493292 ref NP_871742.1	CI protein [Onion yellow dwarf viru	38.5	0.83	G
gi 78368935 ref ZP_00839126.1	ATP-dependent helicase HrpB [Shew	38.5	0.83	
gi 88806214 ref ZP_01121732.1	putative ATP-dependent DNA hel...	38.5	0.86	
gi 53714294 ref YP_100286.1	hypothetical protein BF3005 [Bacter	38.1	0.92	G
gi 95930623 ref ZP_01313357.1	ATP-dependent helicase HrpB [D...	38.1	0.93	
gi 76258862 ref ZP_00766515.1	Aldehyde oxidase and xanthine ...	38.1	0.94	
gi 56480445 ref NP_709628.2	ATP-dependent DNA helicase [Shig...	38.1	0.97	G
gi 15804414 ref NP_290454.1	ATP-dependent DNA helicase [Esch...	38.1	1.1	G
gi 49176420 ref YP_026263.1	ATP-dependent DNA helicase [Esch...	38.1	1.1	G
gi 82546173 ref YP_410120.1	ATP-dependent DNA helicase [Shigell	38.1	1.1	G
gi 82778997 ref YP_405346.1	ATP-dependent DNA helicase [Shigell	38.1	1.1	G

gi 75236871 ref ZP_00720940.1 	COG0514: Superfamily II DNA helicase	38.1	1.1	
gi 75230783 ref ZP_00717246.1 	COG0514: Superfamily II DNA helicase	38.1	1.1	
gi 83858641 ref ZP_00952163.1 	DEAD/DEAH box helicase [Oceanicau...	38.1	1.1	
gi 90581058 ref ZP_01236858.1 	putative ATP-dependent DNA helicase	38.1	1.1	
gi 89074461 ref ZP_01160938.1 	putative ATP-dependent DNA helicase	38.1	1.1	
gi 77813211 ref ZP_00812489.1 	ATP-dependent helicase HrpB [Shew...	38.1	1.1	
gi 83954472 ref ZP_00963183.1 	ATP-dependent helicase HrpB [Sulf...	38.1	1.1	
gi 83943900 ref ZP_00956357.1 	ATP-dependent helicase HrpB [Sulf...	37.7	1.2	
gi 62182427 ref YP_218844.1 	ATP-dependent DNA helicase [Salm...]	37.7	1.2	G
gi 56415812 ref YP_152887.1 	ATP-dependent DNA helicase [Salm...]	37.7	1.2	G
gi 16762176 ref NP_457793.1 	ATP-dependent DNA helicase [Salm...]	37.7	1.2	G
gi 54310561 ref YP_131581.1 	putative ATP-dependent DNA helicase	37.7	1.2	G
gi 109118220 ref XP_001097819.1 	PREDICTED: RecQ protein-like 5	37.7	1.2	G
gi 51242949 ref NP_004250.3 	RecQ protein-like 5 isoform 1 [Homo...	37.7	1.2	U G
gi 25013749 ref NP_734295.1 	CI protein [Barley mild mosaic virus]	37.7	1.2	G
gi 19749339 ref NP_604491.1 	RNA1 polyprotein [Barley mild mosaic virus]	37.7	1.2	G
gi 109118218 ref XP_001098200.1 	PREDICTED: RecQ protein-like 5	37.7	1.3	G
gi 77361487 ref YP_341062.1 	ATP-dependent DNA helicase [Pseu...]	37.7	1.3	G
gi 16767228 ref NP_462843.1 	ATP-dependent DNA helicase [Salmonella]	37.7	1.3	G
gi 85000727 ref XP_955082.1 	DEAD-box family helicase [Theileria...	37.7	1.3	G
gi 72153274 ref XP_787603.1 	PREDICTED: similar to DEAH (Asp-Asn)	37.7	1.4	G
gi 67539314 ref XP_663431.1 	hypothetical protein AN5827.2 [Aspergillus fumigatus]	37.7	1.4	G
gi 24646066 ref NP_524319.2 	mutagen-sensitive 309 CG6920-PA [Drosophila melanogaster]	37.4	1.6	U G
gi 90589729 ref ZP_01245378.1 	ATP-dependent DNA helicase RecQL	37.4	1.6	
gi 90414260 ref ZP_01222240.1 	putative ATP-dependent DNA helicase	37.4	1.6	
gi 68542893 ref ZP_00582614.1 	ATP-dependent helicase HrpB [Shewanella]	37.4	1.6	
gi 82741698 ref ZP_00904413.1 	ATP-dependent helicase HrpB [Shewanella]	37.4	1.7	
gi 68545749 ref ZP_00585299.1 	ATP-dependent helicase HrpB [Shewanella]	37.4	1.7	
gi 83857591 ref ZP_00951119.1 	putative ATP-dependent DNA helicase	37.4	1.7	
gi 83858931 ref ZP_00924570.1 	COG0514: Superfamily II DNA helicase	37.4	1.7	
gi 58393124 ref XP_319843.2 	ENSANGP00000025250 [Anopheles gambiae]	37.4	1.7	G
gi 24372223 ref NP_716265.1 	ATP-dependent helicase HrpB [Shewanella]	37.4	1.8	G
gi 50123092 ref YP_052259.1 	ATP-dependent DNA helicase [Erwinia]	37.4	1.8	G
gi 21224937 ref NP_630716.1 	ATP-dependent helicase [Streptomyces]	37.4	1.8	G
gi 89889904 ref ZP_01201415.1 	ATP-dependent DNA helicase RecQ	37.4	1.8	
gi 91226497 ref ZP_01261246.1 	putative ATP-dependent helicase	37.4	1.9	
gi 109896583 ref YP_659838.1 	ATP-dependent DNA helicase RecQL	37.4	1.9	G
gi 29349252 ref NP_812755.1 	ATP-dependent DNA helicase recQL	37.0	2.0	G
gi 75188564 ref ZP_00701831.1 	COG0514: Superfamily II DNA helicase	37.0	2.0	
gi 75853732 ref ZP_00761505.1 	COG1643: HrpA-like helicases [Vibrio]	37.0	2.0	
gi 17556386 ref NP_497420.1 	Y67D2.6 [Caenorhabditis elegans]	37.0	2.1	U G
gi 88803234 ref ZP_01118760.1 	putative ATP-dependent DNA helicase	37.0	2.1	
gi 89894700 ref YP_518187.1 	hypothetical protein DSY1954 [Desulfovibrio]	37.0	2.1	G
gi 71023321 ref XP_761890.1 	hypothetical protein UM05743.1 [Ustilago]	37.0	2.2	G
gi 77360909 ref YP_340484.1 	ATP-dependent helicase with nucleic acid binding domain	37.0	2.3	G
gi 86140388 ref ZP_01058947.1 	putative ATP-dependent DNA helicase	37.0	2.3	
gi 76638750 ref XP_607648.2 	PREDICTED: similar to DEAH (Asp-Asn)	37.0	2.4	G
gi 86133525 ref ZP_01052107.1 	putative ATP-dependent DNA helicase	37.0	2.4	
gi 66809201 ref XP_638323.1 	hypothetical protein DDB0186395 [Diaphorina citri]	37.0	2.4	G
gi 67469003 ref XP_650493.1 	DEAD/DEAH box helicase [Entamoeba histolytica]	37.0	2.5	G
gi 109896817 ref YP_660072.1 	ATP-dependent helicase HrpB [Pseudomonas]	37.0	2.5	G
gi 109092044 ref XP_001088680.1 	PREDICTED: DEAH (Asp-Glu-Ala)	37.0	2.5	G

gi 50423857 ref XP_460513.1	hypothetical protein DEHA0F03762...	37.0	2.5	G
gi 107026746 ref YP_624257.1	amidophosphoribosyltransferase ...	37.0	2.5	G
gi 74014888 ref ZP_00685516.1	Amidophosphoribosyl transferase [37.0	2.5	
gi 71676318 ref ZP_00674060.1	Helicase, C-terminal:Type III ...	36.6	2.6	
gi 67547355 ref ZP_00425259.1	Amidophosphoribosyl transferase [36.6	2.6	
gi 85713431 ref ZP_01044421.1	ATP-dependent helicase HrpB [Nitr	36.6	2.6	
gi 67468457 ref XP_650264.1	recQ family helicase [Entamoeba his	36.6	2.6	G
gi 73965025 ref XP_540436.2	PREDICTED: similar to ATP-depend...	36.6	2.6	U G
gi 72161116 ref YP_288773.1	helicase, C-terminal:DEAD/DEAH b...	36.6	2.7	G
gi 88859956 ref ZP_01134595.1	putative ATP-dependent helicase [36.6	2.7	
gi 90592069 ref ZP_01247706.1	ATP-dependent DNA helicase Rec...	36.6	2.7	
gi 18485510 ref NP_569721.1	RecQ protein-like 5 [Mus musculus]	36.6	2.8	U G
gi 90407207 ref ZP_01215394.1	putative ATP-dependent DNA hel...	36.6	2.8	U G
gi 20544129 ref NP_068750.2	DEAH (Asp-Glu-Ala-His) box polypept	36.6	2.9	U G
gi 84716398 ref ZP_01023028.1	ATP-dependent DNA helicase Rec...	36.6	2.9	
gi 109492252 ref XP_001081701.1	PREDICTED: similar to RecQ p...	36.6	2.9	G
gi 17552054 ref NP_498895.1	RNA HelicAse family member (rha-2)	36.6	3.0	U G
gi 88792832 ref ZP_01108550.1	ATP-dependent DNA helicase [Al...	36.6	3.1	
gi 91974782 ref YP_567441.1	ATP-dependent helicase HrpB [Rhodop	36.6	3.1	G
gi 76645937 ref XP_603974.2	PREDICTED: similar to ATP-depend...	36.6	3.2	G
gi 78062965 ref YP_372873.1	amidophosphoribosyltransferase [Bur	36.6	3.3	G
gi 89890375 ref ZP_01201885.1	ATP-dependent DNA helicase RecQ [36.6	3.3	
gi 37522198 ref NP_925575.1	ATP-dependent DNA helicase [Gloeoba	36.2	3.5	G
gi 23004116 ref ZP_00047615.1	COG0514: Superfamily II DNA he...	36.2	3.6	
gi 94312259 ref YP_585469.1	ATP-dependent DNA helicase RecQ [Ra	36.2	3.7	G
gi 19074102 ref NP_584708.1	ATP-DEPENDENT RNA HELICASE (DEAD...	36.2	3.7	G
gi 69951291 ref ZP_00639032.1	ATP-dependent DNA helicase Rec...	36.2	3.8	
gi 75674557 ref YP_316978.1	ATP-dependent helicase HrpB [Nitrob	35.8	4.4	G
gi 86148265 ref ZP_01066561.1	ATP-dependent DNA helicase RecQ [35.8	4.4	
gi 84393647 ref ZP_00992398.1	ATP-dependent DNA helicase RecQ [35.8	4.4	
gi 85014143 ref XP_955567.1	pre-mRNA splicing factor [Encephali	35.8	4.7	G
gi 56461347 ref YP_156628.1	Helicase, ATP-dependent [Idiomarina	35.8	4.7	G
gi 55652443 ref XP_514647.1	PREDICTED: hypothetical protein XP	35.8	4.7	G
gi 109645079 ref ZP_01368999.1	DEAD/DEAH box helicase-like [...	35.8	4.7	
gi 77814563 ref ZP_00813821.1	ATP-dependent DNA helicase Rec...	35.8	4.8	
gi 71000850 ref XP_755106.1	mRNA splicing factor RNA helicas...	35.8	4.9	G
gi 88713743 ref ZP_01107824.1	ATP-dependent DNA helicase rec...	35.8	5.0	
gi 54310256 ref YP_131276.1	hypothetical ATP-dependent helic...	35.8	5.1	G
gi 72109102 ref XP_783015.1	PREDICTED: similar to Probable A...	35.8	5.1	G
gi 77739558 ref ZP_00808049.1	ATP-dependent DNA helicase Rec...	35.8	5.2	
gi 58382418 ref XP_311930.2	ENSANGP00000010973 [Anopheles gabi	35.8	5.3	G
gi 85099496 ref XP_960795.1	hypothetical protein [Neurospora cr	35.8	5.3	G
gi 86747631 ref YP_484127.1	ATP-dependent helicase HrpB [Rhodop	35.8	5.4	G
gi 90579760 ref ZP_01235569.1	putative ATP-dependent helicase [35.8	5.5	
gi 77952760 ref ZP_00817173.1	Helicase, C-terminal:DEAD/DEAH...	35.8	5.5	
gi 86131801 ref ZP_01050398.1	putative ATP-dependent DNA helica	35.8	5.5	
gi 41053341 ref NP_956318.1	DEAH (Asp-Glu-Ala-His) box polypept	35.8	5.6	U G
gi 77361139 ref YP_340714.1	ATP-dependent helicase [Pseudoalter	35.8	5.6	G
gi 82495358 ref ZP_00880934.1	ATP-dependent helicase HrpB [Shew	35.4	5.7	
gi 103485877 ref YP_615438.1	peptidase S1 and S6, chymotryps...	35.4	5.8	G
gi 50546625 ref XP_500782.1	hypothetical protein [Yarrowia lipo	35.4	6.2	G
gi 27375353 ref NP_766882.1	ATP-dependent DNA helicase [Bradyrh	35.4	6.4	G

gi 76646513 ref XP_869834.1	PREDICTED: similar to Probable A...	35.4	6.4	G
gi 86360653 ref YP_472541.1	hypothetical protein RHE_PE00379 [R	35.4	6.5	G
gi 68483511 ref XP_714316.1	putative rRNA biogenesis helicas...	35.4	7.0	G
gi 68484077 ref XP_714041.1	putative rRNA biogenesis helicas...	35.4	7.0	G
gi 37520933 ref NP_924310.1	probable helicase protein [Gloeobac	35.4	7.0	G
gi 46137751 ref XP_390567.1	conserved hypothetical protein [Gib	35.4	7.0	G
gi 92118900 ref YP_578629.1	ATP-dependent DNA helicase RecQ [Ni	35.4	7.1	G
gi 33151690 ref NP_873043.1	ATP-dependent DNA helicase [Haemoph	35.4	7.3	G
gi 13473449 ref NP_105016.1	DNA helicase RecQ [Mesorhizobium lo	35.4	7.3	G
gi 85060315 ref YP_456017.1	ATP-dependent DNA helicase RecQ ...	35.0	7.6	G
gi 91794513 ref YP_564164.1	ATP-dependent helicase HrpB [Shewan	35.0	7.6	G
gi 37528437 ref NP_931782.1	ATP-dependent DNA helicase RecQ ...	35.0	7.8	G
gi 83313353 ref YP_423617.1	Superfamily II DNA helicase [Magnet	35.0	8.0	G
gi 88948137 ref ZP_01150900.1	Helicase, C-terminal:DEAD/DEAH...	35.0	8.0	
gi 6323844 ref NP_013915.1	Nucleolar DNA helicase of the Rec...	35.0	8.7	G
gi 39972399 ref XP_367590.1	hypothetical protein MG07501.4 [Mag	35.0	9.0	G
gi 85373654 ref YP_457716.1	serine protease, putative [Erythrob	35.0	9.0	G
gi 71420156 ref XP_811384.1	aminoacylase [Trypanosoma cruzi str	35.0	9.2	G
gi 62326966 ref YP_224077.1	gp1 [Cucumber vein yellowing virus]	35.0	9.3	
gi 74009225 ref YP_308881.1	CI protein [Cucumber vein yellowing	35.0	9.3	
gi 19921526 ref NP_609946.1	CG10689-PA [Drosophila melanogaster	35.0	9.4	U/G
gi 15603292 ref NP_246366.1	RecQ [Pasteurella multocida subsp.	35.0	9.6	G
gi 68249329 ref YP_248441.1	ATP-dependent DNA helicase RecQ ...	35.0	9.6	G
gi 46133102 ref ZP_00156591.2	COG0514: Superfamily II DNA he...	35.0	9.6	
gi 16272669 ref NP_438887.1	ATP-dependent DNA helicase [Haemoph	35.0	9.6	G
gi 94311396 ref YP_584606.1	amidophosphoribosyltransferase [Ral	34.7	9.9	G

Alignments

Get selected sequences Select all Deselect all Distance tree of results

> gi|22129793|ref|NP_671491.1| G polyprotein [Hepatitis C virus]
Length=3011

Score = 1286 bits (3328), Expect = 0.0, Method: Composition-based stats.
Identities = 670/685 (97%), Positives = 678/685 (98%), Gaps = 0/685 (0%)

Query 1	APITAYAQQTGGLGCITSLTGRDKNQVEGEVQIVSTAATQFLATCINGVCWTYHGAG	60
Sbjct 1027	APITAYAQQTGGLGCITSLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTYHGAG	1086
Query 61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct 1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query 121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct 1147	DSRGSLSPRPISYLKGSSGGPLLCPAGHAVGLFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query 181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct 1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266